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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele–specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,
5   the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,
10   generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and
15   is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In
20   many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism
25   (RFLP) Is a variation in DNA sequence that alters the length of a restriction fragment (Botstein *et al.*, *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic
analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell*
51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 85-99
(1989)). When a heritable trait can be linked to a
5   particular RFLP, the presence of the RFLP in an individual
can be used to predict the likelihood that the animal will
also exhibit the trait.

Other polymorphisms take the form of short tandem
repeats (STRs) that include tandem di-, tri- and tetra-
10   nucleotide repeated motifs. These tandem repeats are also
referred to as variable number tandem repeat (VNTR)
polymorphisms. VNTRs have been used in identity and
paternity analysis (US 5,075,217; Armour *et al.*, *FEBS Lett.*
307, 113-115 (1992); Horn *et al.*, WO 91/14003; Jeffreys, EP
15   370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide
variations between individuals of the same species. Such
polymorphisms are far more frequent than RFLPs, STRs and
VNTRs. Some single nucleotide polymorphisms occur in
20   protein-coding sequences, in which case, one of the
polymorphic forms may give rise to the expression of a
defective or other variant protein and, potentially, a
genetic disease. Examples of genes, in which polymorphisms
within coding sequences give rise to genetic disease
25   include β-globin (sickle cell anemia) and CFTR (cystic
fibrosis). Other single nucleotide polymorphisms occur in
noncoding regions. Some of these polymorphisms may also
result in defective protein expression (e.g., as a result
of defective splicing). Other single nucleotide
30   polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same
manner as RFLPs and VNTRs, but offer several advantages.
Single nucleotide polymorphisms occur with greater

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5   polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10   employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15   their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20   both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a

5   polymorphic site. Complements of these segments are also included.   The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying

10   the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These

15   oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table,

20   column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a

25   set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases

30   present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

     An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally

5 occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment

15 of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the

20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

25   Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen *et al.*, *Science* 254, 1497-1500 (1991).

     As used herein, the term primer refers to a single-

30 stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (*e.g.*, in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from
5   15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.
10   The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with
15   the complement of the 3' end of the sequence to be amplified.

     As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same
20   chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

     As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site
25   is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include
30   restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most
5   frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.
10   A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less
15 than 1/100 or 1/1000 members of the populations).
        A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another
20 pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is
25 occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.
        Hybridizations are usually performed under stringent
30 conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
5   identity or similarity between the target nucleotide
sequence and the primer or probe used.

      The term "isolated" is used herein to indicate that the
material in question exists in a physical milieu distinct
from that in which it occurs in nature. For example, an
10   isolated nucleic acid of the invention may be substantially
isolated with respect to the complex cellular milieu in
which it naturally occurs. In some instances, the isolated
material will form part of a composition (for example, a
crude extract containing other substances), buffer system
15   or reagent mix. In other circumstance, the material may be
purified to essential homogeneity, for example as
determined by PAGE or column chromatography such as HPLC.
Preferably, an isolated nucleic acid comprises at least
about 50, 80 or 90 percent (on a molar basis) of all
20   macromolecular species present.

      I.   Novel Polymorphisms of the Invention
      The novel polymorphisms of the invention are listed in
the Table. The first column of the Table lists the names
assigned to the fragments in which the polymorphisms occur.
25   The fragments are all human genomic fragments. The
sequence of one allelic form of each of the fragments
(arbitrarily referred to as the prototypical or reference
form) has been previously published. These sequences are
listed at http://www-genome.wi.mit.edu/ (all STS's
30   (sequence tag sites)); http://shgc.stanford.edu (Stanford
STS's); and http://ww.tigr.org/ (TIGR STS's). The Web
sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms
    A. Preparation of Samples
    Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine,
fecal material, sweat, buccal, skin and hair. For assay of
cDNA or mRNA, the tissue sample must be obtained from an
organ in which the target nucleic acid is expressed. For
5   example, if the target nucleic acid is a cytochrome P450,
the liver is a suitable source.

Many of the methods described below require
amplification of DNA from target samples. This can be
accomplished by e.g., PCR. *See generally PCR Technology:*
10   *Principles and Applications for DNA Amplification* (ed. H.A.
Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A
Guide to Methods and Applications* (eds. Innis, et al.,
Academic Press, San Diego, CA, 1990); Mattila *et al.,*
Nucleic Acids Res. 19, 4967 (1991); Eckert *et al., PCR*
15   *Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson
et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase
chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560
(1989), Landegren *et al., Science* 241, 1077 (1988),
20   transcription amplification (Kwoh *et al., Proc. Natl. Acad.*
Sci. USA 86, 1173 (1989)), and self-sustained sequence
replication (Guatelli *et al., Proc. Nat. Acad. Sci. USA,*
87, 1874 (1990)) and nucleic acid based sequence
amplification (NASBA). The latter two amplification
25   methods involve isothermal reactions based on isothermal
transcription, which produce both single stranded RNA
(ssRNA) and double stranded DNA (dsDNA) as the
amplification products in a ratio of about 30 or 100 to 1,
respectively.

30   B. Detection of Polymorphisms in Target DNA
There are two distinct types of analysis of target DNA
for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is
carried out to identify polymorphic sites not previously
characterized (i.e., to identify new polymorphisms). This
analysis compares target sequences in different individuals
5   to identify points of variation, i.e., polymorphic sites.
By analyzing groups of individuals representing the
greatest ethnic diversity among humans and greatest breed
and species variety in plants and animals, patterns
characteristic of the most common alleles/haplotypes of the
10 locus can be identified, and the frequencies of such
alleles/haplotypes in the population can be determined.
Additional allelic frequencies can be determined for
subpopulations characterized by criteria such as geography,
race, or gender. The de novo identification of
15 polymorphisms of the invention is described in the Examples
section. The second type of analysis determines which
form(s) of a characterized (known) polymorphism are present
in individuals under test. There are a variety of suitable
procedures, which are discussed in turn.

20   1. Allele-Specific Probes
        The design and use of allele-specific probes for
analyzing polymorphisms is described by e.g., Saiki et al.,
Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki,
WO 89/11548. Allele-specific probes can be designed that
25 hybridize to a segment of target DNA from one individual
but do not hybridize to the corresponding segment from
another individual due to the presence of different
polymorphic forms in the respective segments from the two
individuals. Hybridization conditions should be
30 sufficiently stringent that there is a significant
difference in hybridization intensity between alleles, and
preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are
designed to hybridize to a segment of target DNA such that
the polymorphic site aligns with a central position (e.g.,
in a 15-mer at the 7 position; in a 16-mer, at either the 8

5   or 9 position) of the probe. This design of probe achieves
good discrimination in hybridization between different
allelic forms.

Allele-specific probes are often used in pairs, one
member of a pair showing a perfect match to a reference

10 form of a target sequence and the other member showing a
perfect match to a variant form. Several pairs of probes
can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the
same target sequence.

15   2. Tiling Arrays
The polymorphisms can also be identified by
hybridization to nucleic acid arrays, some examples of
which are described in WO 95/11995. One form of such
arrays is described in the Examples section in connection

20 with de novo identification of polymorphisms. The same
array or a different array can be used for analysis of
characterized polymorphisms. WO 95/11995 also describes
subarrays that are optimized for detection of a variant
form of a precharacterized polymorphism. Such a subarray

25 contains probes designed to be complementary to a second
reference sequence, which is an allelic variant of the
first reference sequence. The second group of probes is
designed by the same principles as described in the
Examples, except that the probes exhibit complementarity to

30 the second reference sequence. The inclusion of a second
group (or further groups) can be particularly useful for
analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur
within a short distance commensurate with the length of the
probes (e.g., two or more mutations within 9 to 21 bases).

         3. Allele-Specific Primers
5   An allele-specific primer hybridizes to a site on
target DNA overlapping a polymorphism and only primes
amplification of an allelic form to which the primer
exhibits perfect complementarity. See Gibbs, *Nucleic Acid
Res.* 17, 2427-2448 (1989). This primer is used in
10   conjunction with a second primer which hybridizes at a
distal site. Amplification proceeds from the two-primers,
resulting in a detectable product which indicates the
particular allelic form is present. A control is usually
performed with a second pair of primers, one of which shows
15   a single base mismatch at the polymorphic site and the
other of which exhibits perfect complementarity to a distal
site. The single-base mismatch prevents amplification and
no detectable product is formed. The method works best
when the mismatch is included in the 3'-most position of
20   the oligonucleotide aligned with the polymorphism because
this position is most destabilizing to elongation from the
primer (see, e.g., WO 93/22456).

         4. Direct-Sequencing
         The direct analysis of the sequence of polymorphisms of
25   the present invention can be accomplished using either the
dideoxy chain termination method or the Maxam Gilbert
method (see Sambrook *et al.*, *Molecular Cloning, A
Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind
et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30   1988)).

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5.   Denaturing Gradient Gel Electrophoresis
      Amplification products generated using the polymerase
chain reaction can be analyzed by the use of denaturing
gradient gel electrophoresis. Different alleles can be
5   identified based on the different sequence-dependent
melting properties and electrophoretic migration of DNA in
solution. Erlich, ed., *PCR Technology, Principles and
Applications for DNA Amplification*, (W.H. Freeman and Co,
New York, 1992), Chapter 7.

10   6.   Single-Strand Conformation Polymorphism Analysis
      Alleles of target sequences can be differentiated using
single-strand conformation polymorphism analysis, which
identifies base differences by alteration in
electrophoretic migration of single stranded PCR products,
15   as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86,
2766-2770 (1989). Amplified PCR products can be generated
as described above, and heated or otherwise denatured, to
form single stranded amplification products. Single-
stranded nucleic acids may refold or form secondary
20   structures which are partially dependent on the base
sequence. The different electrophoretic mobilities of
single-stranded amplification products can be related to
base-sequence differences between alleles of target
sequences.

25 III. Methods of Use
      After determining polymorphic form(s) present in an
individual at one or more polymorphic sites, this
information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set
of polymorphic sites in an individual identifies a set of
polymorphic forms that distinguishes the individual. *See*
5 *generally* National Research Council, *The Evaluation of
Forensic DNA Evidence* (Eds. Pollard *et al.*, National
Academy Press, DC, 1996). The more sites that are
analyzed, the lower the probability that the set of
polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are
analyzed, the sites are unlinked. Thus, polymorphisms of
the invention are often used in conjunction with
polymorphisms in distal genes. Preferred polymorphisms for
use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be
determined with greater accuracy than those of multiple
polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set
of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood
sample from a suspect matches a blood or other tissue
sample from a crime scene by determining whether the set of
polymorphic forms occupying selected polymorphic sites is
the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a
sample, it can be concluded (barring experimental error)
that the suspect was not the source of the sample. If the
set of markers does match, one can conclude that the DNA
from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci
tested have been determined (e.g., by analysis of a
suitable population of individuals), one can perform a
statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given
5   polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism is (see WO 95/12607):

10 Homozygote: $p(AA) = x^2$
Homozygote: $p(BB) = y^2 = (1-x)^2$
Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the
15 probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$

These calculations can be extended for any number of
20 polymorphic forms at a given locus. For example, the probability of identity p(ID) for a 3-allele system where the alleles have the frequencies in the population of x, y and z, respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for each of multiple unlinked loci is determined by multiplying
30 the probabilities provided by each locus.

cum $p(ID) = p(ID1)p(ID2)p(ID3).... p(IDn)$

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The cumulative probability of non-identity for n loci
(i.e. the probability that two random individuals will be
different at 1 or more loci) is given by the equation:
cum p(nonID) = 1-cum p(ID).

If several polymorphic loci are tested, the cumulative
probability of non-identity for random individuals becomes
very high (e.g., one billion to one). Such probabilities
can be taken into account together with other evidence in
determining the guilt or innocence of the suspect.

B.   Paternity Testing
The object of paternity testing is usually to determine
whether a male is the father of a child. In most cases,
the mother of the child is known and thus, the mother's
contribution to the child's genotype can be traced.
Paternity testing investigates whether the part of the
child's genotype not attributable to the mother is
consistent with that of the putative father. Paternity
testing can be performed by analyzing sets of polymorphisms
in the putative father and the child.

If the set of polymorphisms in the child attributable
to the father does not match the set of polymorphisms of
the putative father, it can be concluded, barring
experimental error, that the putative father is not the
real father. If the set of polymorphisms in the child
attributable to the father does match the set of
polymorphisms of the putative father, a statistical
calculation can be performed to determine the probability
of coincidental match.

The probability of parentage exclusion (representing
the probability that a random male will have a polymorphic
form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$p(exc) = xy(1-xy)$

where x and y are the population frequencies of alleles A
5   and B of a biallelic polymorphic site.

(At a triallelic site $p(exc) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)))$, where x, y and z and the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is
10 $p(non-exc) = 1-p(exc)$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$cum\ p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3)....$
15 $p(non-excn)$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$cum\ p(exc) = 1 - cum\ p(non-exc)$.
20 If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's
25 polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits
The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and
30 contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell
mutation confers resistance to malaria, but a homozygous
sickle cell mutation is usually lethal. Other
polymorphisms occur in noncoding regions but may exert
5   phenotypic effects indirectly via influence on replication,
transcription, and translation. A single polymorphism may
affect more than one phenotypic trait. Likewise, a single
phenotypic trait may be affected by polymorphisms in
different genes. Further, some polymorphisms predispose an
10   individual to a distinct mutation that is causally related
to a certain phenotype.

Phenotypic traits include diseases that have known but
hitherto unmapped genetic components (e.g.,
agammaglobulimenia, diabetes insipidus, Lesch-Nyhan
15   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome,
Fabry's disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrand's
disease, tuberous sclerosis, hereditary hemorrhagic
telangiectasia, familial colonic polyposis, Ehlers-Danlos
20   syndrome, osteogenesis imperfecta, and acute intermittent
porphyria). Phenotypic traits also include symptoms of, or
susceptibility to, multifactorial diseases of which a
component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
25   system, and infection by pathogenic microorganisms. Some
examples of autoimmune diseases include rheumatoid
arthritis, multiple sclerosis, diabetes (insulin-dependent
and non-independent), systemic lupus erythematosus and
Graves disease. Some examples of cancers include cancers
30   of the bladder, brain, breast, colon, esophagus, kidney,
leukemia, liver, lung, oral cavity, ovary, pancreas,
prostate, skin, stomach and uterus. Phenotypic traits also
include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance,
fertility, and susceptibility or receptivity to particular
drugs or therapeutic treatments.

    Correlation is performed for a population of
5   individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a κ-
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

    Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the
possibility of transmitting such a polymorphism from her
husband to her offspring. In the case of a weaker, but
still statistically significant correlation between a
5   polymorphic set and human disease, immediate therapeutic
intervention or monitoring may not be justified.
Nevertheless, the patient can be motivated to begin simple
life-style changes (e.g., diet, exercise) that can be
accomplished at little cost to the patient but confer
10   potential benefits in reducing the risk of conditions to
which the patient may have increased susceptibility by
virtue of variant alleles. Identification of a polymorphic
set in a patient correlated with enhanced receptiveness to
one of several treatment regimes for a disease indicates
15   that this treatment regime should be followed.

For animals and plants, correlations between
characteristics and phenotype are useful for breeding for
desired characteristics. For example, Beitz *et al.*, US
5,292,639 discuss use of bovine mitochondrial polymorphisms
20   in a breeding program to improve milk production in cows.
To evaluate the effect of mtDNA D-loop sequence
polymorphism on milk production, each cow was assigned a
value of 1 if variant or 0 if wildtype with respect to a
prototypical mitochondrial DNA sequence at each of 17
25   locations considered. Each production trait was analyzed
individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF
percentage, energy concentration, or lactation energy
30   record; μ is an overall mean; YS_i is the effect common to
all cows calving in year-season; X_k is the effect common to
cows in either the high or average selection line; β_1 to β_{17}
are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent
environmental effect common to all records of cow n; a_n is
effect of animal n and is composed of the additive genetic
contribution of sire and dam breeding values and a
5   Mendelian sampling effect; and e_p is a random residual. It
was found that eleven of seventeen polymorphisms tested
influenced at least one production trait. Bovines having
the best polymorphic forms for milk production at these
eleven loci are used as parents for breeding the next
10 generation of the herd.

    D.   Genetic Mapping of Phenotypic Traits
    The previous section concerns identifying correlations
between phenotypic traits and polymorphisms that directly
or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage
between a genetic locus associated with a trait of interest
and polymorphic markers that are not associated with the
trait, but are in physical proximity with the genetic locus
responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated
with a phenotypic trait to a chromosomal position, and
thereby cloning gene(s) responsible for the trait. *See*
Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357
(1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337
(1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)).
Genes localized by linkage can be cloned by a process known
as directional cloning. *See* Wainwright, *Med. J. Australia*
159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).
    Linkage studies are typically performed on members of a
family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5   segregate with a phenotypic trait. *See, e.g.,* Kerem *et al., Science* 245, 1073-1080 (1989); Monaco *et al., Nature* 316, 842 (1985); Yamoka *et al., Neurology* 40, 222-226 (1990); Rossiter *et al., FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10   odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ, versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15   Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20   ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the $\log_{10}$ of this ratio (i.e., a lod

25   score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30   scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. *See*

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Smith *et al.*, *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate

5   of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod

10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.

15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV.   Modified Polypeptides and Gene Sequences

20   The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some

25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)

30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown
in the Table.

Variant genes can be expressed in an expression vector
in which a variant gene is operably linked to a native or
5   other promoter. Usually, the promoter is a eukaryotic
promoter for expression in a mammalian cell. The
transcription regulation sequences typically include a
heterologous promoter and optionally an enhancer which is
recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic
enzyme promoters and tRNA promoters, depends on the host
selected. Commercially available expression vectors can be
used. Vectors can include host-recognized replication
systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and
the like.

The means of introducing the expression construct into
a host cell varies depending upon the particular
construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction,
electroporation or injection, as described in Sambrook,
supra. A wide variety of host cells can be employed for
expression of the variant gene, both prokaryotic and
eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian
cells, typically immortalized, *e.g.*, mouse, CHO, human and
monkey cell lines and derivatives thereof. Preferred host
cells are able to process the variant gene product to
produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond
formation, general post-translational modification, and the
like.

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The protein may be isolated by conventional means of
protein biochemistry and purification to obtain a
substantially pure product, *i.e.*, 80, 95 or 99% free of
cell component contaminants, as described in Jacoby,
5   *Methods in Enzymology* Volume 104, Academic Press, New York
(1984); Scopes, *Protein Purification, Principles and
Practice*, 2nd Edition, Springer-Verlag, New York (1987);
and Deutscher (ed), *Guide to Protein Purification, Methods
in Enzymology,* Vol. 182 (1990). If the protein is
10   secreted, it can be isolated from the supernatant in which
the host cell is grown. If not secreted, the protein can
be isolated from a lysate of the host cells.
     The invention further provides transgenic nonhuman
animals capable of expressing an exogenous variant gene
15   and/or having one or both alleles of an endogenous variant
gene inactivated. Expression of an exogenous variant gene
is usually achieved by operably linking the gene to a
promoter and optionally an enhancer, and microinjecting the
construct into a zygote. *See* Hogan *et al.*, "Manipulating
20   the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor
Laboratory. Inactivation of endogenous variant genes can
be achieved by forming a transgene in which a cloned
variant gene is inactivated by insertion of a positive
selection marker. *See* Capecchi, *Science* 244, 1288-1292
25   (1989). The transgene is then introduced into an embryonic
stem cell, where it undergoes homologous recombination with
an endogenous variant gene. Mice and other rodents are
preferred animals. Such animals provide useful drug
screening systems.
30   In addition to substantially full-length polypeptides
expressed by variant genes, the present invention includes
biologically active fragments of the polypeptides, or
analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active
fragments include any portion of the full-length
polypeptide which confers a biological function on the
variant gene product, including ligand binding, and
5   antibody binding. Ligand binding includes binding by
nucleic acids, proteins or polypeptides, small biologically
active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that
specifically bind to variant gene products but not to
10   corresponding prototypical gene products are also provided.
Antibodies can be made by injecting mice or other animals
with the variant gene product or synthetic peptide
fragments thereof. Monoclonal antibodies are screened as
are described, for example, in Harlow & Lane, *Antibodies, A*
15   *Laboratory Manual*, Cold Spring Harbor Press, New York
(1988); Goding, *Monoclonal antibodies, Principles and
Practice* (2d ed.) Academic Press, New York (1986).
Monoclonal antibodies are tested for specific
immunoreactivity with a variant gene product and lack of
20   immunoreactivity to the corresponding prototypical gene
product. These antibodies are useful in diagnostic assays
for detection of the variant form, or as an active
ingredient in a pharmaceutical composition.

V. Kits
25   The invention further provides kits comprising at least
one allele-specific oligonucleotide as described above.
Often, the kits contain one or more pairs of allele-
specific oligonucleotides hybridizing to different forms of
a polymorphism. In some kits, the allele-specific
30   oligonucleotides are provided immobilized to a substrate.
For example, the same substrate can comprise allele-
specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.
10   The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15   EXAMPLES
     The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.
30   A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect
complementarily with one of the reference sequences. Each
probe in the first probe set has an interrogation position
that corresponds to a nucleotide in the reference sequence.
5 That is, the interrogation position is aligned with the
corresponding nucleotide in the reference sequence, when
the probe and reference sequence are aligned to maximize
complementarily between the two. For each probe in the
first set, there are three corresponding probes from three
10 additional probe sets. Thus, there are four probes
corresponding to each nucleotide in the reference sequence.
The probes from the three additional probe sets are
identical to the corresponding probe from the first probe
set except at the interrogation position, which occurs in
15 the same position in each of the four corresponding probes
from the four probe sets, and is occupied by a different
nucleotide in the four probe sets. In the present
analysis, probes were 25 nucleotides long. Arrays tiled
for multiple different references sequences were included
20 on the same substrate.

Multiple target sequences from an individual were
amplified from human genomic DNA using primers for the
fragments indicated in the listed Web sites. The amplified
target sequences were fluorescently labelled during or
25 after PCR. The labelled target sequences were hybridized
with a substrate bearing immobilized arrays of probes. The
amount of lable bound to probes was measured. Analysis of
the pattern of label revealed the nature and position of
differences between the target and reference sequence. For
30 example, comparison of the intensities of four
corresponding probes reveals the identity of a
corresponding nucleotide in the target sequences aligned
with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the
nucleotide occupying the interrogation position of the
probe showing the highest intensity (see WO 95/11995). The
existence of a polymorphism is also manifested by
5   differences in normalized hybridization intensities of
probes flanking the polymorphism when the probes hybridized
to corresponding targets from different individuals. For
example, relative loss of hybridization intensity in a
"footprint" of probes flanking a polymorphism signals a
10   difference between the target and reference (i.e., a
polymorphism) (see EP 717,113). Additionally,
hybridization intensities for corresponding targets from
different individuals can be classified into groups or
clusters suggested by the data, not defined a priori, such
15   that isolates in a give cluster tend to be similar and
isolates in different clusters tend to be dissimilar.
Hybridizations to samples from different individuals were
performed separately. The Table summarizes the data
obtained for target sequences in comparison with a
20   reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention
includes a number of general uses that can be expressed
concisely as follows. The invention provides for the use
of any of the nucleic acid segments described above in the
25   diagnosis or monitoring of diseases, such as cancer,
inflammation, heart disease, diseases of the CNS, and
susceptibility to infection by microorganisms. The
invention further provides for the use of any of the
nucleic acid segments in the manufacture of a medicament
30   for the treatment or prophylaxis of such diseases. The
invention further provides for the use of any of the DNA
segments as a pharmaceutical.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and

5   individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAAACTCCACTTGAAGCCAAAGAAAGAAGAAACTCACACTTAAAACACATGCCAGTTGGGAAGGTCT GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	---	⋮	TACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAATGCTGTGTCTCTGTCAG AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATTGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAGCCCCTAGGATTTAGATACAATCTTGAAAGAAAACTGAGACAGATAATTCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-10744	61	G	C	---	⋮	GGGCAAATTACCAGCAAAAAAGTCAAATTACCAGCATCAAAGTGCAAAGGAGGTAGAACAA TTACAGTAACTATGTCAATCTTTTTGTTATATTAGTATCTGCCCAATGCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCTTTTTCTTCCCTCTTCATTCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATGTATCAATTGATTCTTACTGA
WI-9975	126	C	T	---	⋮	GCTAGGTTTGTTCTGTTGGCGTGTCTTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT GATGTAACTAGTCTGAGACCTTCCCTCTCCGCAATTCCCAGGTTTCAGAAAGTATGCCACAC TCAACCCTTCTCTCCAGTTCATCCTGTATTAATTCTTCCCATATTAATTCAAAGGGAGTTGGACAGGT CCCTGGCTGAAAAGAAAATAAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-8010	247	G	T	---	⋮	GCCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTTTCTCCATCCTAGGATTCTGCCTATAAT CTTTGTCCTGTGTA[G/C]ATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTGCTCTTGAATTTTCTCTGCTATTGAGGACATTCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-5222b	85	G	C	---	⋮	GCCCGGCCTATCTTTAATTTAACTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGTCCTGTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTGCTCTTGAATTTTCTCTGCTATTGAGGACATTCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-5222	52	G	C	---	⋮	TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTATTATTACTAACTATAGTCCTTCTTGGAAGGAACACCCAAACCAATACTT ATAAAGTACATGTAATTTATAGTAACATATTTACTATACATATGGAAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-8007	242	C	A	---	⋮	TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTGTTTGTTAG TCTATATTCACACATATGAGTGAAATTTC[C/T]GGGGCATGGGAAATACATCTTTATGACACATTGA ACTGCTCACCACCATCATCAGTATCCATTAAACAGACCAACAACATGTATAAGAATTCCCTTTGTTTTAC
WI-9823	97	C	T	---	⋮	ATGCTTTCCAATCTGATTTGTATGACTATTGTGCACAGTTGGATCACC

Marker	Position	Allele 1	Allele 2	Sequence
WI-9651b	105	A	T	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCCTACTTGTCCTCCATGTACAATTTTCTGCTCGTCCTTCA[A/T]GGGGCAGCTTGCAAGCCTCCCTTAGACACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCCAGGGGACCCTTATAGGCCTCTGTCTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-9651	139	T	C	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCCTCCTCTGGAATTCCTTCCTACTTGTCCTCATGTACAATTTTCTGCTCGTCCTTCAAGGGGCAGCTTGCAAGCCTCCCTTAGACACCTC[T/C]ACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCCAGGGGACCCTTATAGGCCTCTGTCTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-7676b	309	A	C	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGGACTTGGCCCTGCTATTTATTTTGTATTTATGTCTTAATCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAAGGGGCCGGCCTTCTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGCTCCCCCGGCCTTCTCCTCCTGGAGGCAGTATAGGAGAGAGAGAAGGCAAGGATT
WI-7676	139	C	T	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGGACTTGGCCCTGCTATTTATTTTGTATTTATGTCTTAATCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAAGGGGC[C/T]GGCCTTCTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGCTCCCCCCGTCTCCTCCTGGAGGCAGTATAGGAGAGAGAGAAGGCAAGGATT
WI-10072	105	G	A	CATTATCTTGTCCTTGGGTCTCGTGTTCATTCACTTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCATTCATCTGGCCCTTTTTGAGTTTGAATATTTTTGT[G/A]TGACTCCTATGCACATGATAAATTTGTTATGCTTGTCTCTTATCTTTGTTATAGGAGTTTTGGCCATGACCCTTTATGAGGAGAAAAAGGGATCACCCCCTTTTGCCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T	C	TTGGTGTGAACTCAGAATATAGGGAGAAAATAAGACAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAGCCCTGCACTTGACTCCAAAAGGAGTTCTATTATTCTGGCTGTTCCAGACTTATTGTATCTTGAGAAGAGAACTGTTTTCCCTCTAAATCAGTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCAATATCAATAGCATGCATATGGGGTGTTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C	A	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGAGGGCCTGCACATGCAAACTCCAGTCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTTCAGGGCTTTGCATGCGCTCTATTCCCCCTCTGCCTCTGC[C/A]CCACCTTCTTTGGAGCAAGGAGATGCAGCTGTATTGTGTAACAAGCTCATTTGTAACAGTGTCTGTTCATGTAATAA
WI-7224	134	T	C	ATAAACCCTTGTGTATCATGTGTATCACCCAACTCACTAATTATCAACTTATGTGTCTATCAGATATCCTCTCTACCCTCACGTTATTTTGAAGAAAATCCTAAACATCAAATACTTTCATCCATAAAAATGTCAGCATT[T/C]ATTAAAAAACAATAAACTTTTAAAGAAAACATAAGGACACATTTTCAAATTAATAAAATAAAGGCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGAGTGATTCATGCTAG

ID	Pos	Alleles	Sequence
WI-10826	132	A C	TCTTATTTGCATTCACAGTAGCCCATGAAGTAGGTATAACCAGCCTCTATTTTAACATGAGAAGAT GGAGGCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCCTAATAAGCAAAGACCTGCA[A/C]]CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTCCTGTCAGCCCAGACCCCATGCGCA GAAAGCCCAGCCTCTCCATCCCCAC
TIGR-A004S25	145	G A	AGATCTGCCATTAGTATTATTCCTTGAAGATACTTTGGAGATTCATTTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAAACTTGTGGGGTATAGAAATGGAAGAGTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCCTTAGGCATTGAAACCATCACCTGGTTGCATTCTTC ATGACTGAGGTTAACTTAAAATGACTGAGGTTAACTTAAAAC
WI-1021	24	A T	AACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTAGTATTATCATTCCTGTAATAGATTCACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAAACTCTCCGTACTGTAATTTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTTGGTTTCCAC
WI-4687	121	G T	TAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTGAATGGTCTTGTCC TTTCAATAAAAAGAGTGACACATGATTGAACATGTGTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCCACTGGATAATCTAAAAAACCAAGAGAAGAAGAAACTTGAT
WI-4719b	107	T G	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT ATGTCTGACGCCATGGGTGTTCATAAGTGACTTGAGAGT[T/G]ACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCATTCAACAATTCTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTCATAAGTGACTGAGAGTTACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCATTCAACAATTCTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C	TCAACACGCTTTATTGCCACTTCTGGCTCCCCTCGTCCCCAGCAAGATTCCTACCTCTTACCCTGTAGG AATACTGAGCTCGGATCGCAGGGGAATGGGGTGGGGGGTGTTACCACTTCTCTCTGCCACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGAGGGAGGGGCCAGACAGGGAGGAATTCCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCCAGTTTCCAAACTTT
WI-9484	178	G A	TCAACACGCTTTATTGCCACTTCTGGCTCCCCTCGTCCCCAGCAAGATTCCTACCTCTTACCCTGTAGG AATACTGAGCTCGGATCGCAGGGGAATGGGGTGGGGGGTGTTACCACTTCTCTCTGCCACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGAGGGAGGGGCCAGACAGG[G/A]AGGAATTCAAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCGAGAGTATAGGGACCAGGGTTCCAAACTTT

ID	No.	Alleles	Sequence
WI-7330	207	C T	AGGATGGAAGGAGACACGGGCAGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACGATGGTTGGCTGGTGAATTTCTTCTTTAATTGTGGCATATAGGTTT GTGACACAAGAAGTCATACTTTGGTGGCTAAGTTTTACTAAGGAAAATAACTGAAAAGATTAAAAG TGAGAG[C/T]TGAAAAGAGAAATGATAAATGCTTCCAAACTGTAGCTGTCACAG
WI-9443	211	G A	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAGGGATGTGATTACAATTTAAATGAATCAGTCACTT GCACAATTAATCCTCTTGGCATCATCATACAAACTGGGTTTAATGGCAAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACCTGAGGGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCACCAATGCCCACTT
WI-7166	59	C T	TCTCTCAAAAGAGAAAAACAAAACCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTAAACTTGTTGCTGTGAACAATTGTCGAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C, C	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCGAGTTCCTCTCTGAGTTCCTCTGGGCT GCGCAGGCGGCTCCCCTGGGAATAGAGCAAGACGTGAGTCGTAACCTGGCCACAGT[C/G]TGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGCGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G T	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCGAGTTCCTCTCTGAGTTCCTCTGGGCT GCGCAGGCGGCTCCCCTGGGAATAGAGCAAGACGTGAGTCGTAACCTGGCCACA[G/C,T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGCGCCCAACTTCCCCTGGAGC
WI-7322	275	A G	GTACTTTAGGCTGTGTGGAGGGTGGGCATTTAGTGGTGACCCTTGCACCAGGGTTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTGCCCTCTCTCACCCTATATG GCCATAAAACTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTGACCAGAGAAAGAAGCACTC TGGTTCTCTATCCCCTTGTCACATAGAGAGTTTGTCATGGGGCCCTCTGGCTG
WI-7685	46	T C	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC[T/C]TTTTCTCCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCAACAGAGTGCTTTCTGTCTC CTGGGGTTGAGCTGTGTGCCTCAGTCGGGGCTGTTGCCTCAGTCGTGTCTC
WI-563	87	G A	TGTGACCAATTGTTATTTTAGAGGGTTAACAATGGCCTGACTATCACCTGATGGTCGCCGCAGAATTTC CTGGGGGAGGGCCTCCCCTG[G/A]CCCTGATCATGTCTAACTGCCTACTCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCTCAGTAAAGGCAAATTTTAAAAATCTCTTTGGATAACCCAGGGCACAT

Name	Pos			Sequence
WI-931c	191	C	A	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCTGGAGTTTCTCTCCCCTCCCATCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCTGTTGCTGCACTGTCATTACTGTTGTATGGATTATAATTATTGTCCAAAAAAGCC[C/A]CGAGCCTGGTACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-931b	81	A	G	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCTGGAGTTTCTCTCCCCTCCCT[A/G]TCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCTGTTGCTGCACTGTCATTACTGTTGTATGGATTATAATTATTGTCCAAAAAAGCCCCGAGCCTGGTACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-931	31	A	G	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCTGGAGTTTCTCTCCCCTATCCCTCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCTGTTGCTGCACTGTCATTACTGTTGTATGGATTATAATTATTGTCCAAAAAAGCCCCGAGCCTGGTACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-10870b	91	C	T	GGATGACTTACCCAATAGCAGAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGAGACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTACTTAGAGAGCAGTGGAGTACCCTGAGTACGACCCCCTTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGCCTGAGCCACTCTTAAACATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103	G	A	GGATGACTTACCCAATAGCAGAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGAGACATCCACCTTAGCAAAGTGGGGCACCTACTACTTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCCTTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGCCTGAGCCACTCTTAAACATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281	T	C	AGTTTATTCTTCCAGATGACCAGCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTTGGGAAATATTTGGGCATTGGTCTGCGCCAAGTGTCTACAATGTCTACACGGTCTCATGAGCAATAATGTGTCTTAGTGAAGACAATGTACAGTTATCATTAGATCAAGACTACACGGTCTCATGAGCAATAATGTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATTTCAAGCTAAAGCAA
WI-7719	163	A	G	AGTTTATTCTTCCAGATGACCAGCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTTGGGAAATATTTGGGCATTGGTCTGCGCCAAGTGTCTACAATGTCTACACGGTCTCATGAGCAATAATGTGTTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTCATGAGCAATAATGTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATTTCAAGCTAAA
WI-10396	72	C	A	GCCCTGGGAGTATATCTCAAACTGTGGCCTCCACTTCATTTTCTTGAAACATTGCTATCAACTGGGAAGAGTT[C/A]T[G/A]TGACTTTATGCCCAGTTTCCCCTCTCCAGATTTTTATGACGGTTGTTTTCTTTTGTTATGCCATTTGAGGGATTGAGGATGTTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTCAGGTTAACAGCCACCATTTGTAAACACTTTGT

ID	Pos	A1	A2	Sequence
WI-10673	94	C	G	TCCCTTTATGCACCCAAGAGATATTTATTAAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCCGTGGCACTCATGGAGGGGG[C/G]TGCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGGCCCCCTGCCCCAATTCAATCCTGCCAATAAATCCTGCTCTTATTGTTCATCCTG GAGAATTGAAGGGAGGTCAAGTTGTTTGTCAATGATTTGTCAGAGAACCT
WI-7842	57	T	C	CACAGCCATGCCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCCTATCCCATTCTG[T/C]GTATGAG TCCCATTGCCTTGCAATTAGCATTCTGTCTCCCCAAAAAAGAATGTGCTATGAAGCTTTCTTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGAATTCAGCTCCCTTATA
WI-7721	145	A	C	CTGCCCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGCCACATCCCCACCCCAGCGTTACCCGGGGCAGGTGCAGCCCTTCCTCCC TGTCTCTGC[A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCCTCTG TGTCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173	C	A	TTTCCAGTCTGTTTTATCCTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGTATGTT CTTGCCTTGAGAAATCCTAGAAATCCTAGAAAGCACACAGGGATGACA[C/A]AAATCACTAAGGAATTCCACTAAGA CTCCTCTAACCCAGAGATTTTTAACCT
WI-4767	50	A	G	TTTCCAGTCTGTTTATCCTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGTATG TTTCTTGCCTTGAGAAATCCTAGAAATCCTAGAAAGCACACAATCACTAAGGAATTCCACTAAGAC TCCTCTAACCCAGAGATTTTTAACCT
WI-7718f	222	C	T	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAA AGGAACAAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAAACTATGTATTAAT
WI-7718e	60	T	C	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTC AAAAGGAACAAAAAATTACAAAGAACCATGCAGGAAGGAAAAACTATGTATTAAT
WI-7718d	31	G	A	ATTGCACTGAAGTTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTC AAAAGGAACAAAAAATTACAAAGAACCATGCAGGAAGGAAAAACTATGTATTAAT

WI-7718c	91	C	G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTC AAAAGGAACAAAAAATTACAAAGAACCATGCGACAAAACTATGTATTAAT
WI-7718b	248	A	G C	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAA AGGAACAAAAAATTACAAAGAACCATGCGACAAAACTATGTATT[A/G]AT
WI-7718a	42	A	T	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C,T]GTTACTCCCTACACTGATGC AAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAG TCAAAAGGAACAAAAAATTACAAAGAACCATGCGACAAAACTATGTATTA
WI-7227d	99	G	C	AGGGAATTGTGTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAACAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G	A	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAACAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G	T	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A	G	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCAGTAGGTCACCTGGC TTCCGGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A	C	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCTGTGTGATCCTTCATCGTGTGATGCGAAAACTCCG AAGAGGAAGCAAGAAAGCCGTACTACTGTCTATGTTGTGATCCTTCATTGTAATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAAGGACATGTCTATTGAACTGCTAATTGCCAAACACTGTAAAT ATCCACAGACTCCCTGCCCCATCCCA[A/C]ATGATCTTGAGATTC

ID	Pos			Sequence
WI-7310a	64	T	A	CCACAAATGCCTCTCCCACGATGTCAAGGACTCCTGTCGTGCTGGAGGTGGGAGACAAGGAACC[T/A]CCGAAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATGCAACAAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAAGGACATGTCTATTGAACTGAGCCAAACACTGT AAATATCCACAGACTCCCTCCCCTGCCCCCATCCCAAATGATCTTGAGATTTC
WI-7878b	162	A	G	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGAGGGCAAATGCGTCC CTGAGGAGAAAATCTGGGAGGAGCTG[A/G]TGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGT CTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7878a	51	C	G	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATAA TCAGATCATGCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGAGGGCAAATGC GTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7381c	213	C	T	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGAGCAGGCTGCCTATGGTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCTC[C/T]GGCTCTCGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C	G	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGAGCAGGCTGCCTATGGTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCTCGCGGCTCTCGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C	G	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGAGCAGGCTGCCTATGGTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCTCGCGGCTCTCGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G	A	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
WI-1017a	92	G	A	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

WI-1795b	130	T	C	⋯ GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTAAATTGTATGCATTTCACCAAATTCGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTGCAGAAAGAAAG[T/C]CGTCTACCATTTCACCAAATTCGTGAGTACAAATTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAAAGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T	C	⋯ GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGT[T/C]CTTCCAGACTCCTACGATTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTGCAGAAAGAAAGTCGTCTACCATTTCACCAAATTCGTGAGTACAAATTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAAAGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G	A	⋯ CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTATCACATTGCCAC[G/A]TAGCCCTCCCTTCCCTTCCCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616c	136	G	A	⋯ CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTATCACATTGCCAC[G/A]TAGCCCTCCCTTCCCTTCCCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616b	141	C	T	⋯ CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTATCACATTGCCACGTAGC[C/T]CTCCCTTCCCTTCCCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616a	116	G	C	⋯ CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTACTTCCACGTCTCTCCATACGTAGGTCCTG[G/C]TCTCCTATCACATTGCCACGTAGCCCTCCCTTCCCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-1126c	52	G	A	⋯ CTCTTATTTCTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCACT[G/A]ATACTAATATAAAAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATCAGATTGTTTCCCAGCAAAGAAAATTTTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCCTCAAAAGGAATATGAAATTTGTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
WI-1126b	230	T	C	⋯ CTCTTATTTCTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCACTGATACTAATATAAAAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATCAGATTGTTTCCCAGCAAAGAAAATTTTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCCTCAAAAGGAATATGAAATTTGTTAAAATGCAAATCCAGCTGTAACTTTT[T/C]GGACTTGTCTTTATTTCTT

			Sequence
WI-1126a	97	T C	CTCTTATTTCTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCCACTGATACTAATATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGAT[T/C]CAATATATATCCAGATTGTTTCCCAGCAAAGAAA ATTTATTTCTCAAGATATAAAAAAATAAAATAATTAATTTCAGTTCCTCAAAGGAATATGAAATTT GTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTTATTTCTT
WI-11183c	124	C T	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGT[C/T]ACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACTAACATTT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAA[T/C]ATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGC[C/T]CTTGTCACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	GCTTGGTTTGCTTATTGTCTCAGTGTCTTGAGTTCTCCCTTTCTGCCTGGCCCTTTTGTATTCA CCCATACCTCTATGCCTCGTCTCAGACCATTCCTCATCTGGAGCGCTCTTCCTTGTACTTTCCTG TTCACCAACCTCTTCTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-10770a	49	G T	GCTTGGTTTGCTTATTGTCTCAGTGTCTTGAGTTCTCCCTTTCT[G/T]CCTGGCCCTTTTGTATT TCACCCATACCTCTATGCCTCGTCTCAGACCATTCCTCATCTGGAGCGCTCTTCCTTGTACTTTCTC CTGTTCACCAACCTCTTCTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-9667b	82	C T	GATGACAACTTGCTGTGACCCTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTAAACCTTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G C	GATGACAACTTGCTGTGACCCTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATG[G/C]TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTAAACCTTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

ID	Pos			Sequence
WI-10400d	189	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGAGACATCTGCTGGTTAACTGTTATAAGATGGTTTAGCACACACCCCCAAAATATTCAAAGGCGTTAATGCATTATTTTCTTTCCCTTACCTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG[A/G]TGCCATGTAG
WI-10400c	166	A	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGAGACATCTGCTGGTTAACTGTTATAAGATGGTTTAGCACACACCCCCAAAATATTCAAAGGCGTTAATGCATTATTTTCTTTCCCTTACCTTACTTCCCCCACCA[A/C]AAATAACGTAAGTAAGGCGTTAATGCATTATG
WI-10400b	165	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGAGACATCTGCTGGTTAACTGTTATAAGATGGTTTAGCACACACCCCCAAAATATTCAAAGGCGTTAATGCATTATTTTCTTTCCCTTACCTTACTCCCCCACCC[A/G]AAAATAACGTAAGTAAGGCGTTAATGCATTATG
WI-10400a	46	T	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAA[T/C]TGCATTCAGACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACTTACTCCCCCAAAATAACGTAAGTACCTATGTCATGCCATGTAGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACACCCTCTCACCA[C/T]TTAGAAAAGGGCATTCAAGCACATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATAGGCTTAA
WI-10809a	33	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAA[C/T]GGTATAAGGAGGGTAAATGCAAGGGGAGACCCCACCTCTCACCACTTAGAAAAGGGCATTCAAGCACATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATAGGCTTAA
WI-7038c	266	T	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGCCCAGACAAGAAGACTGTCAGGAAGGGTCGGAGTTGGCTTTTTCACATTGAT
WI-7038b	140	A	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGCCCAGACAAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAAACCAGCATACAGTTGGCTTTTTCACATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	CGAGCTTGGGGATAAAGCAAGGGACCTTGGC[G/A]CTCTCAGCTTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCCTTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAAGATCCTGCATTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	ATACGCTTTCTGTCTGTCCCACAGTGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCGCCCCTTCAGCTTGCATGTCCAGTGTCCTCCTGGCTCAGCAGCAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCCTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	ATACGCTTTCTGTCTGTCCCACAGTGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACAC[C/T]AG CCCTCAGCGCCCCTTCAGCTTGCATGTCCAGTGTCCTCCTGGCTCAGCAGCAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCCTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAAGTGAGTGACGGTGACCT GTGAGCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAA[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCCATTTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCTGAAT TTCATATATACCTCCATTATTTATTCAATACATCATTGCCAAGACAAAAGCAACGGTGCCAACTGGGTT TGGTTGGTTGGTCCTGCACACCCACA[G/T]TTGGCAACTAAGTAAGTCAATCTCTAAA
WI-6711a	36	T C	---	GGCTATTTGTAAATGCTTGGTATTTGACTCCAAAA[T/C]TGAATAAGTAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCCATTTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCT GAATTTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGCAACGGTGCCAACTG GGTTTGGTTGGTTGGTCCTGCACACCCACAGTGGCAACTAAGTAAGTCAATCTCTAAA

WI-10613b	172	A	C	ATTGTATGCCAAAATCATATACCCTGCATTCTAGAAACATACAGTGTAATAGAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACGTTTAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G	A	ATTGTATGCCAAAATCATATACCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACGTTTAACATCAATGAATGTG ATTTTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGGATGTAG
WI-7587c	133	A	T	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTG[G/A]ATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCTGAGGAAA T]GGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCT TTCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587b	81	G	A	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGA AGCACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587a	28	C	T	ATGACTCAGGTGACAAAGAAGAAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTTAAAAAAGCCT[T/A]AAAGACAGCCATTTAATCCTAATTCCG TAGTTTATGATTTTCTCAAAATTTGTCTTTGGAGAAGGAGTGACGCTCTGTTAAAG CCATTGCTAACACTATTGTCTTTGGAGAAGGAGTGACGCTCTGTTAAAG
WI-10681b	103	T	A	ATGACTCAGGTGACAAAGAAGAAGCATGTCCTAGACCCCATTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTAAAGACAGCCATTTAATCCTAATTCCG TAGTTTATGATTTTCTCAAAATTTCAAGGTTCTAAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGTGACGCTCTGTTAAAG
WI-10681a	41	A	T	GCCTCTCCTCCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTTGAACAAGAAGAAGAACTTCAAGGTAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT
WI-7222c	126	G	T	

ID	Pos	Allele 1	Allele 2	Sequence
WI-7222b	255	G	A	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCCTGTTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGGAATTCCCTGAACAAGAGAACTGGGATAGTTATATTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGGAATTCCCTGAACAAGAGAACTGGGGATAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTT
WI-8054d	41	C	A	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTTCTT[C/A]TTATCTCCTCCCAGTTCAAAATG CTTGCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTTCTTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G	T	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGA[G/T]AATCCTTGCCCTT
WI-8054b	148	T	C	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGT[T/C]TTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C	G	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAAGACGATAGTTAACGTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACAGGG[G/T]GGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	C	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG

Marker	Pos					Sequence
WI-9826b	127	G	A	...		AATTTATATGTGAAGGGTTAGCAAACTATGGCCCACCAGAGGCCCATTCTTAGCCATGCCTATTTTTGTG TGCCTGATGGCTGTTTGGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATG[G/A]GCCTT CAAAGCCAAAAAAAAATTTACTCTCTGGCCTTGACGGGGAAAGTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTTGAA
WI-9826	125	A	T	...		AATTTATATGTGAAGGGTTAGCAAACTATGGCCCACCAGAGGCCCATTCTTAGCCATGCCTATTTTTGTG TGCCTGATGGCTGTTTGGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTT[A/T]TGGCCTTC AAAGCCAAAAAAAAATTTACTCTCTGGCCTTGACGGGGAAAGTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTTGAA
WI-15986	60	T	G	TTTGTTTGTGT GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGGTTTGTTGTGTGTGGGTTTTTTTTTT[T/G]TTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A	G	AACTGCAAAT AGGAAACCAG AG	CCACCTGGGGC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAG[A/G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGGAGGAGGTGGCCCTACACCCTTAT
WI-8170b	259	G	A	...		GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T	A	...		GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C	G	CCTTTATTAAA ATTGTTTTCTT GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAGTCATCTTCCAATACTCCAGGTCACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAAACAAGCTTTAAAATCCTTCGGTAACTCCCTTATTAAAATTGTTTTCTTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTTCACCGTTTACA
WI-8183	56	G	A	TGAAATAAAA ACAATTTCTGT TGC	TGTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTCAACACAGTTGAATCTGTAAAAACCAAAGCTCGTTTCTGATGCAGGACAAAATATCCACAAT ATTTAAAAACTGCAAGCACCATGC
WI-14149	83	C	T	...		GCTTTATTGGGATTGCAAGCGGTTACAAGGTTAAAGACAAAACCCAAGCATGGGATTTTGCCGGAAAT ATTAGCGTTAAAGGAG[C/T]TTGAGTTGAGTCAAACACGGG
WI-8712	44	G	A/G	CACAGGGAAG AGGTAGTGGA G	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCTTAACCAGCAGACCCCAGCAACCTAGAAGCGCCTCACCTAGCCTCTAAT

ID	Pos	Allele			Sequence
WI-8827	22	C T	TCCCCTGGGAG ACTATGG	GCGATTAGGAT TTAGTGTTCA C	GGTGTCCCCTGGGAGACTATGG[C/T]AGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTTCTTATCCACCCAGTCTTCT
WI-8833	51	A T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTTCCATGCCATTCTCTG[A/T]TGCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAGGTCAGCTATGT
WI-8377	63	A G	...	...	ATTTTTAGCCATGTTGGTAAAGTTCATTTTCAGTACATGGGTAACACCCAGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTTGTTGTCTAATGTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCCT	CAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGGCTGTTGGCCTGCCTTGCTGCTGCGT TCTTCTTACTGGTCTTTCCTTGTTCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79	C T	CCCGGGCATTG AGGATA	AGTCTTCCTGA GCCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCCTTAGCTTCGTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A G	...	...	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGGAGTCGAGCTTTCCATATAAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGGAGTCGAGCTTTCCATATAAA
WI-8895	32	A C	...	...	GTGCCACAAACCTGACACCAACCAACAGAAT[A/C]CTCCCGTCCTTTGAAATTTCCATTAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G C	...	...	CCTTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAAATATAATAAAACTCTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTAATATAAACATTTCTAAGTGTCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCACACGGCAACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCAAACTCCCGTCTCAAAACTCGGTCTCAGTCACCCAC
WI-8496b	157	A G	...	...	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGACCTAGAAATCAGAGCAGCACTAGTATACAAG AAGACACAAATGCTGCCAATGCA[A/G]TTAGTTATATAGAAATAATAACGAGCTGTTAGAAAAGTCT GTGGCCAAGTGGGATAAAAACAGTAGCAGTGCAC
WI-8496	41	G A	...	...	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCACTAGTGTCAAGTAGTATACAAG GTCAAAGACACATGCTGCCAATGCAATTAGTATATAGAAATAATACGAGCTGTTAGAAAAAGTC TGTGCCCAAGTGGGGATAAAAACAGTAGCAGTGCAC
WI-14153	28	A G	GTGCAGGAAG GCCAGC	AACGGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCTCCTGCGTGTCACCCACAGAGCA GCCCTAGTGCCCAGGTGCCACTGCCACCCACGCCGGGAACAGGAGACCCATGCTGC

ID						
WI-12108	40	C	T	TGGAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[C/T]GAAATACTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29	G	A	CCACAAAGGT CACAGGCA CG	GGGTATAACAG AACCGTATGTA CG	CAGGCAAACGTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTCATTTTAGTGTATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTTTCTTGGGTGAGGACACC
WI-12201	61	C	T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTTCCTGGAGTGTTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTCGGGGTGTGATGGACGTGGGTTTGCAGCCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A	T	GGCAGCCAGC TCTGACTT AG	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A	G	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAGGC	TTTTTCGTTTGTTTAATGATCCGAATGCTTGAGAAGAAACCCTGGCCTCGCTGCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A	G	CATGCCCTTTA AGGATTAAGT TT	TCTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTATTTATTGATTGGTATATTCAGGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAAGAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T	C	GTTGAGTATTT GTTCTGTCTCAT AATT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATCAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATT[T/C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G	A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTCAAAC CTGTTTGCATTTGAAATCAAACAAAGTTAGCGTTTTTGTAAATCAAATTGATAACCCGACTAAAAAT
WI-12361	63	C	T	---	---	TTAAATTCCACACTGAAGATCTGAGTATGGGGGGGATATAGGAATTTCAGCATATGTATTATC[C/T] TGAACTAAATTTACAAAGTGGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C	T	CAGACACAGC ATCACACCA	GACCCTCCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCAGCATCCACACCA[C/T]AGGGCCCACGGGGAGGGTCGGGGAGACGACACTTTCCCTGGG AAAGG
WI-11321	67	A	G	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAAATCTTTAAGCAGGAGGGAGGAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCCG
WI-11324	40	C	G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]GAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTTGTCC

Name	No.	A	B	Primer 1	Primer 2	Sequence
WI-11352a	69	T	C	AGCACAGCACATAGTGGAAAG	GACCTCGTAGGACACTTAGCCACTTA	TGACACATGGTTTCTGTTTCCAGAAGGAGAGAGAGAAGTCATCTCACATAAGCACAGCACATAGTGGAAAG[T/C]GCTAAGTGTCCTACGAGAGATCATATCCATAGAAAAAACAGCTCTCTTTACTTGCA
WI-11371	84	C	T	CAGCTTGGAGATTCTGATTCAG	GCCCCGCCTGAGCAC	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAAACTATACCTGCCCAGGCTCAGCTTGGAGATTCTGATTCAG[C/T]GTGCTCAGGCGGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGTGATTTCGATGCGTATAT
WI-11385	75	T	C	ACAGAAGACTTTCATATTCTTGTTTTT	GATTCTATTCTAGTCATGGTCATATTTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTTCATATTCTTGTTTTTAAAAGTCTCTTCAGT[T/C]AGGAAAAAGCTACAGATTTAAAAAATATGACCATGAGAATAGAATCAGC
WI-11388	88	C	A	TGTTTGAAATTACACGTAACTAAGTTC	TGCCTTGTATCCAAGTTAAAATT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAATTAAAGAATGAATGTTTGAATTACACGTAACTAAGTTC[C/A]ATAAATTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T	G	GGTTATGTGTTCTTGAACTTAATAAATAC	GTACATTCACGTGTTTTTGTAAAAAG	TTCTATCATTCCATTAAAATGGGCAGGTTATGTGTTCTTGAACTTAATAAATAC[T/G]CTTTTTACAAAACACGTGAATGTACTTTTCTTGTCAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGTCATACTCCTTCCCCAGA
WI-11396	52	A	T	TTTTGTTTTTGAAATGGTGTTTT	AGCTTATTTCATATTCACCCATC	AAAGAATAAGATGGCATTTGTTCAGTTAATTTGTTTGAAATGGTGTTT[A/T]GATGGGTGAATATGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C	A	TCCCCACCAACCAGC	TGCCAGGGCCTTATTTG	CTGTCAGTCTTTCCCAACTAACGTGAGTTCCAGTATGTCCAGTCCAGCACGTCTCTTGCTTCTTGGTGTATTCCCATTACTGAATCCCCACCAACCAGC[C/A]CAAATAAGGCCCTGGCACAAAGTAAGCTCTCCAITTTGTAGAATGAAT
WI-11466	26	C	T	TGAGAAGCCATTTATTTTGCA	GTTTATTGTTATAAAAATGACCTACAACTT	ACTTTGAGAAGCCATTTATTTGCAG[C/T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAATTTTTTATATAAGTTGTAGGTCATTTATAACAATAAACTTCTATTATCTATTTATCTCTCACATACATTTCATGTATCCTG
WI-13364	35	A	G	...	...	TTTTTCTTTGTGCTCTTTTTTTTAGTAGAAGC[A/G]GGAACACTGCTTGTCAATACTACCTTCTGTTGGTCCCCTGTTGAGACAACATACCTTTCTTTGAAATGTAAAATGTCA
WI-11276	41	A	G	GGCAGCCAGGAGCAGAC	TGTACTGAGGAGCCGGTG	AGGCAACACTGCTTTATTAGGCCGGGGCAGCCAGGAGCAGCAGCA[A/G]CACCGGCTCCTCAGTACACATTCCCCCACCCCGTGCTCGGGTCCCCACTCAGGGCATGGGCAGCGTAGGGGCAGCGTAGGTCTGGAA
WI-12210	76	A	G	ACTGGGAAAACAACTATTGCA	TGCTAGTTTGCATATGTTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAACAACTATTGCCATA[A/G]GGAAAACATATGCAAACTAGCAACTAGCATCATTGTCTCTAGA
WI-14186b	88	A	G	...	...	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACACATACGGTACAAAATTACAGGTGGTTTAGTTCATTACATG[A/G]TACAAATCATTACAAGTCATTAGAGTCTTTGGATTTT

WI-14186a	52	C	T	GGTCATTTGAT GGAAAGAGACAC A	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTCTGGTTTTATTGATGGAAAGACACTGTTGGTCATTTGATGGAAAGACACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTCATTACATGATGACAAATCATTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAAGAGAACACTTGTGGGGGCTT[A/TGTGGGGCTTA GTTCAAACATGGACTGGATAGGTCCCACCCCCAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGCGCACTTGTGAGATTTGCAAAA
WI-13416	71	C	A	AAATTTTGG AAGTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTCAAATTTTTGGAAGTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAAATATTGAAATATTCATTGAACTATAAACACTTAGCAGAGGAAGGGACTTTGAT
WI-12310	46	G	A	TTATTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGGTCCT AAA	TTTGAAAAGATGCTGAATTATTCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAATTTCAGTTTACAAATATTCCAGAAGGCATTTCTTAAGCAG T
WI-12086	72	C	T	CCGGGAAAAC TTTGGATTT	GGAGTCTTCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAAGAGTGTGGACACTGTTACAACAAAACGTTCCGGGAAAACTTG GATT[C/T]CCAAGACCCGAAGACTCCTCCAAGTTCTCCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTATTTGTTAAGAGTTTGTCTATCTAAATTTCATATTTATTGGCATAAAGT TCATAATATTCTTTTATGATCTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTCCTC
WI-11585	79	T	C	TGGGTTTGCAA CCATGCTTCAC AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAACACGGTAATGGGAAATCAGTTCAGTGGCCTAGGAAGTCAAGAGCTGGGTT TGCAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGCCTAGAGAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	...	...	TTAGTTGGTTCCTGAAACTTTATGCTGTTTATTTTAACCAATAGGATGTTCCAGTTACCAGCATTT[G/C]AGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAATTCTGACGCTCACCATTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C	A	GGACTTCGT	...	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCCACCCTGGACTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTG[A/G]GG CATGTTCCCACCCTGGACTTGCCAACTTCCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	...	...	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTTAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAAAATTGGCAATGA

Clone	Pos.	Allele 1	Allele 2	Flank 1	Flank 2	Sequence
WI-11626a	39	G	A	TCCACTGGAA CATGAAGGTA G	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAAATAAATTACTTAATTAGCCATACCACATTGTTCCATTTGCTAC AAGAACAAATTGGCAATGA
WI-11627	23	T	C	CCTTTCCTTCC ATTGTCCTC	CATTGCAACC CATCTCAAG	ACCCCTTCCTTCCATTGTCCTC[T/C]CTTGAGATGGGTGCAAATGGGAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
WI-11636	61	A	G	GGACTTAAAA AGATCTGCTTA TCCT	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
WI-11537	119	C	G	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCATC[C/G]ATAATCATTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G	C	GCCAAAAGAC TATTCAGCAA CCTG	GGCTCTCCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTCAGCAACTG[G/C]AAACTGTCCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTCATATTTT ATTTTGGGTGTGTGGGT
WI-11656	28	G	A	ATTGATTTTAG AAGGAACTGC AA	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAAATGTCCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T	C	...	...	ACAGATACTTTTCCACGCAACATTCTGAAATGAAAGCTTTGATTCTCCCCTTTT[T/C]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T	C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAACAAAGATACTTTGACATCTTTATCCACAGGGGACAGT[T/C]AAGGTTGGCTTCTA ATGCCCACCACCATCTTGTGTTTCAGAATCTTTCCCACTCGCC
WI-11702	69	C	T	GAATAATACT GAAATAACCA CAGCAG	AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTCAATAATTAAAAATCGAATAATACTGAAATAACCACAGC AG[C/T]TTTCAGTATAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTTGTTCTGCAGA
WI-11706	60	C	T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTTGTACAATTTATTTGC[C/T]GGCTG GAATTTGTCTTGGTGATTTGTCCCCTTGCTGCT
WI-11709	105	T	A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C	A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACAACGCCAGCCAGCCCACACTCAACACGCCTTCAC TCCAGTCGTTCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCCTCCTCCCACACACTCCTTC

Name	Pos	A1	A2	Seq A	Seq B	Seq C
WI-11715b	123	C	T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGGGACATGCACACAATGTAAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A	C	GCACACAATG TAAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGGGACATGCACACAATGTAAAACAGACAAAATGCATTACAACTGTGG TGGTGTAATGTGGCCACTACTGAATCCCTATGTATAAGAGGAAAGAGGGCTGGCTGCAGCTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G	C	AACAATCCTT AAAACAACTA	CCTGTGGGTTG TGTTGCAG	CTGGAATTCCTATACCTAACAATCCTTAAAACAACTATCAACA[G/C]CTGCAACACAAACCACACAGGC AAAATGAAAAACAGATGCCCCAGCAGCACCCCACCACATGGCACAC
WI-11728	16	C	G	...	TGTTCAACA	TTTTATTATCAAAACT[C/G]CAATTCCATTCACAAATGTAAGTTATCATCAGCTCCCCATCCCACTTT CTCCCATCTTCTTATCTCTTCCCACCCTACACTTTCTCTCCCCTACAACCCGGGTTCCAAA
WI-11758	61	A	G	ATCTGTGGTTT TCGCCTG	TGATTGGCCCT GTGGTCTA	TTTTTCCTCTTTTTATTAAGTCCGCTATACTAACTAGAAGGAGAATCTGTGGTTTCGCCTG[A/G]TAG ACCACAGGGCCAATCACCACAGCTTCTTGTGAGAAACATGGAGAGTGCCAAGATCACCATCA
WI-11295	37	A	G	GCCTCACAAA GTATTTCTAA AATATAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGCCTCACAAAGTATTTCTAAAAATATAATTTGCTA[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAACAAATCACTATTGGCTCAGCAGGAAACAGACTTT
WI-11773	93	T	C	...	...	AGCACATGATGATATATTCTGCCTGGAGTTTTCTGTGAGTTTTCTGTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC ATTTATTGCCTCCTTTTTTTCCCCCT[T/C]GTGATTGTTAATTAATGGCTCAGGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA
WI-11282	42	C	G	GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTT GTGTG	CATGACAAACCTCTCTTATTAATGGGCTCAGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGCGCGGAGAGACCCCTCCACCTTTTCATGCCTGTGTGTACACACACTGTCCAAGCCTC AGA
WI-11790	28	A	G	CCCAACTTACC AAACCCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAAACCCTCTGT[A/G]GCTTAGCCTGACTACACACATGCTCAGAGCAC TTACATTAACCTACACATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C	A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTAATTCCCAAAGCTTACAACCATCTCTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AAGT TTTTAATTCCCAAAGCTTACAACCATCTCTTTCATCTAATCTGTGAGGTATTTAGTATACAT GATTTCTCTCTTTCCTTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C	T	GTTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTTCCATTTCTCCCCTTTTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA ATGTGGCTTATATTCTATTTGTTGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52	A	G	TGTTTATAACAT CAAAGAAAGA ATCTGAA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAGAAAGAATCTGAAT[A/G]TGAGGGAACTG CAGAAATTAAACTTTCAGTGTCTAATTCTCAGAATGCCAGAGTGAAGATGAACCCTTTACAG

Marker						Sequence
WI-11909	78	A	G	TTTGTTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAGAGACAATGGATTGTGGAGCATACTGAAGAGACTATTCCTAAATGGCTATTGTGTTG GGTGGTCAAG[A/G]CTATTCAGAAAATCTCAGAAAATGATGCACTGCAGCCAGCTCG GACTGGCTTGCAAGAGTC
WI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C	A	---	---	CCCTAGTGAATACAACCTTTGTCCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT ATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ AATT]GATCAACATTCACCACAGCTGAAGGAAATTAAACTGAACCT
WI-11027	90	T	A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAA[T/A]AATAAAAATACTGTAACACATTCCTCATTTCTCTTACGA ATACTTTCTTTTTGATATTGCAAATTCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95	C	T	---	TTTCCATCTTA TTTCATTTCTG TAAC	TTCTGCTGAAGATCACAAAAACAAATTCAACCTCTGTGGTTCAAAATAATTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGA[C/T]AGACTTCAGAAGGCATAGCTTCCCTTGTAACGTTTTT AAACATCTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69	C	T	AAAAGGACAG CCAGATATCA AC	---	CAACATTTATCAAACATGGTAGGGAAAAGTTCTCACTCTGCACTATAAAAAGAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAACAAATTG
WI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACCTTTCCCATTTACAGACAAAACCAGT
WI-11070b	135	C	T	---	---	ATGAGACCCTGCTTTGAACGTTTAAACGTTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCGAGAGAGGTACTCCAAGTA C[C/T]GTGGGGGTTCTGATGACTTCCACGCGTCACTGGGGATCCAACAGAAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTTGAACGTTTAAACGTTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTT[G/T]GGTGCGAGAGAGGTACTCCAA GTACCGTGGGGGTTCTGATGACTTCCACGCGTCACTGGGGATCCAACAGAAGGGAA
WI-12020	121	T	C	---	---	AATCTTTATATTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCCTC

ID						Sequence
WI-11076b	142	G	A		...	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTTGGGAGGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAAGGGGAGGCATGTCACATACCCAGAGCAGGAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTGTCAT G
WI-11076a	106	T	C	AAGGGGGAGC AGGCA	TCCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTTGGGAGGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAAGGGGAGGCA[T/C]GTCACATACCCAGAGCAGGAGGAGAGA GAGAAAGAGAGGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTGTCAT G
WI-14263	49	T	C	CGCAGAAAAA GGCATATTCA GACA	GGTTATTCAAA AATTAGTATGG	ACCTTTAAAGTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]T[T/C]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-14267	28	T	C		...	AATTATTGCTGAAATTAGGAAGGGAGGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAGAG ATTTAAAAGAAGCAAGTACCATTTCCAAGTATAAAACTCGTA
WI-13892	50	G	A	CTTTTCATTTT TGCTTTTTAAA TAGAAC	TGATGATGTCA TATACTAAAA ATCAAAG	GATTTGTTTATTCATTCTCGCTTTCATTTGCTTTTAAATAGAACA[G/A]CTTGATTTTTAGTA TATGACATCATCATCATGAATTTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	C	G	CATGAGAGGA TTCCCTCTCTC	AAAAGCTTCTT TCCCTTGGA	ACCTCTTCTGATGACACTTGTACCTGTAAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGC TACAAATTCAGGATGCAGGGCATGCAGGGGATTCCCTCTC[C/G]TTCCAAGGGAAAGAAGCTTTTGGC
WI-13951b	88	G	C		...	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGAGGAAGAG GCTTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C	T	GGAGTGAACA AAGTAATGAA CAAAA	TTCCTCTGATC TGGGGTCT	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G	A	AAAAAGGCTC TTGCCCAT	GGAGGGAGAG ACGGGAATA	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATTCCGTCTCTCCCTCCTGACTGACCCCAGTGTTCTT ACAATGAAACATCCCTCAGCCCCATGGCATGGTGCATCCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCAATGGC
WI-13960	39	A	C	AGCAAAAGGA AGTTAAATAC TGATAGA	CATGAAAGAA CAAATTTGCAT C	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAATTTGTCCTTTCATGCA TTTGTGGAGCAAAGTACTAACTTGTTCACTGTCATTTCCCCTCACAAGGAGTTGAGCCCCTAGATGAC
WI-15843	62	C	T	ATCTTATAACC AAGAAGCCTT CAG	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGAGTTTATCACACTTTGTCCTCAGGGTCCACCAGGAACCAGGAGTTCTTGGCT

ID	#					Sequence
WI-13983	52	G	A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCAGTGG	TTGTGTATCTGATTCCGAAACATAGAAATCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGGAATATGCACTCACTAGAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A	G	AATCTCAGGG TCACAGCTTTA TT	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATTTTATAGATTTTTAACACAGCCAT[A/G]TTACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGTGTAAAAAGATTACACTTCA
WI-15295	27	G	C	TGTCAGTTTGA ATGTATTCCTG A	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGAAAATATGAGTGAGACTCA
WI-14284	55	C	T	---	---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAAATAAAATGCTTATCCAGTGAGCGGCTCCCTGATGCATTGA
WI-14288	85	G	C	CCGCTGCTATT CCCAGAT	GGTCTCCTTCC ACCAAATCTT	ATGACCAGACCAGAAGCCCGTGTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAGGACCATGACAGATGACAAACGG
WI-13522	33	C	T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T	C	CACAAACATT TATTGAACAG TTACCA	TCTATACACTT CTCACTCTCT GCTT	AAATATGATTCCATTCCACAAACATTATTGAACAGTTACCA[T/C]AGTTACCACCACCCTC ATAGAGGTGATTTAAGAGTGGTCCCGTCCCTGTCCCTGGGGGTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G	A	---	---	TGAAAGGATACAGAAAAAACTCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCCTCTCCCAGTGCCATTACACTGGAGTACACTTAATTTTCTCAGCA
WI-13536	29	T	C	---	---	TTTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTCCTTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13373	52	G	A	---	---	TTGGTTTTAATACCTCTTGTTGGATAAAAAGGACATTGTTTTCATTAGCTTGTCTTCAAA[A/G]GAC AGAGAAATAAGATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477b	61	A	G	GAAGACAAGC TAATGAAAAA CAATG	---	TTGGTTTTAATACCTCTTGTTGGATAAAAAGG[A/G]CATTGTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A	G	TTAATACCTCT TGTTGGATAA AAGG		

Marker	No.	Allele	Flanking sequences
WI-14297	86	A / T	AATGTTGGGT ACTTTTCCAA G · TGTGCACATTC AGAAACATTTT AAACAGTCGACT · CTGACTTTATTTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATAATGTGCAGTTATAAAAAT GTTGGGTACTTTTCCAAG[A/T]AAAATGTTCTGAATGTGCACACTAGAATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89	T / G	CATGTGCACA AAAAGAGTAA AAA · ACATGTGAATT GTCCCAAAAA AAAT · TCCATGTAAATATTCTCAACAGAGAACACTATCTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAAGATTTTTGGGACAATTCACATGTTC AAAAT
WI-13582	43	C / A	TGCAATCTAG AGACTGGGGA · TCTGCGCAGTT AGATTCCA · AAGGCTGCCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA[C/A]TGGAATCTAACTGCGCAGAG AAATCAAAGACCGATGGTGTGAAATCTGGGGCAGCTTCAAAATTTCTGCCTCCTAAAACATTTCAC CCAATTTTTCATTATTGCC
WI-13857	28	A / G	··· · ··· · TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCCATTTTTGTGTAGCTTTCATACAGTACAGATTTCATTGATGTCGCTCCCACATCTG
WI-15809	77	T / G	TAAGGTAGCTA ATTCAATGTT GTAAA · TGGTTTCTGT TGTAAATGCC · GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCCT[T/G]TTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123	A / T	··· · ··· · TTAATCAGTCTGTGTCAAGAAGAAACAGAACTTGATCAAGCTTCCAGCCCTCACCACTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTGTTGTTTACATTTGTCTAAAACCAGAGAAGGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T / G	CATACTCCACT CTAGCTGCGAGT AA · AGAAGAGTGG ATGGGATGC · TCTTTATTCCAAGAATGGGAAGCGCATTTCATTGGCTTGAATGAGAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCCACTCTTCTTCTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G / A	TTTATTCCAAG TCATTCAAGCC · AATGGGAAGC AATGAAAATG · TCTTTATTCCAAGAATGGGAAGC[G/A]CATTTCATTGGCTTGAATGAGAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCCACTCTTCTTCTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T / C	GGCTGGACACT GCAGTGAT · CCCACACCTGC CCCT · GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGAT[T/C]AGGG GCAGGTGTGGGGGACGGCAGGCCTCGGGGGCCTCTGCGGAGGACGCAAATGTCATGGCAGAGCTTCCAGAA
WI-13578	48	T / A	TCAATAAAGA GCAGAAAGAA AACC · CAGTGTGTAAG AACATCTTTTT GTC · TTTTTTTGGTGAGTGTTTGTCTTCAATAAAGAGCAGAAAGAAAACC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTACACAGTCACCCAAACATTGATATTTGCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCCAGAAACCTC
WI-13789	62	G / A	TTGGATGGCTG AGGGGAG · CAGTGCGCTTC CTCTGTTC · TCCAAGGAAAAAAGAAGAAAAGAAAAACCAATCAGTGAGAAAACTCAAGAATTGGATGGCTGAGGGG[G/A] GAACAGAGGAAGCGCACTCGGGGACTGAATATGGACAGTGGATGGTAGGGTCCTCACTCTCTT GAGGTCCCT
WI-13594	66	G / A	TTTTAACACA GATCACAAAA AGC · CCTTTGGCCCA GTACTTTTT · AATAACAAGTTAAGTTCGAGCTGCAATGTTGGCAATGGCAGGTTTTAACACAGATCACAAAAAGC[G/A] TGCACAAAAAAGTACTGGGCAAGGACAAAATAATAGCTAAGAATTAGGCCAAGCTGC

ID	Pos	A1	A2			Sequence
WI-15625	40	C	T	...	...	GTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGTCCCATACTAATTTTTGAATAACCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C	G	CCACACTGAA GACTCACCAG A	TCCCACCCCA CCCT	GTCTCACTTTCTTGTCTAGGCTGTAAATTTCAGTTAACAAGTTCTTATGTGATTGTGGCCACACTGAAGACTCACCAGAA[C/G]AGGGTGGGGGAATACTTAATCAATATTTGTGGAATTTACCGATGAAATCCAGTATTCCT
WI-13600	26	G	T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTCAATATGCACATTATATTACTGGAAACAAAGAATACGGATTGTGTAGGGAAGACATAGAGGACCACCATCAGCAACCCTCT
WI-13602	89	G	T	TCCATTCTGGA GACAATACA	GCATACCTCAT GACAATATTA ATATTAAT	GATAGGAAAAGAAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCCCTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATATTAAATATTGTCATGAGGTATGCACCT GCCCA
WI-13650	76	A	T	AAAGATTCAC AATATTTCACT TTTAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTAAAAATTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTTCAC TTTTAAAAC[A/T]TAAAAAAACTACTCTTCATATCCTAGTGATGACTTAAAGTTACCGG
WI-14319	83	C	T	CAATTCAAGG CACAAAGCTA A	CCAAATCATCT ATATTGTTGCA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAATAGCAATTCAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTGGGGGTGGGACAGTACAGAATT
WI-13528	80	A	G	CAATACATTT GCATTTCCTA GAAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTAAACTGTAATCAATACATTTGCATTTCCTAAAA[A/G]TTCAGAGAAAAACTGTGGTATCATGCAGGAAAGCAGAAAAAATT
WI-13909c	93	A	T	...	...	ACTTAAACTGGCTTATCTTCACGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACTCGAATATCTTTTC[A/T]GAGATGTCTAGTAGTCTCAGCTAGTACCCACTGCAACATCTCAA
WI-13909b	80	G	A	TTCCTCACACT CTCTTCAAACT C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACT[G/A]AATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCAA
WI-14323b	86	C	A	...	...	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAGGGACAGAAAATTAAGAATCAAACATCATTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACTA
WI-14323a	78	T	C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAGGGACAGAAAAATTAAGAATCAAACATCA[T/C]TCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACTA
WI-15389b	104	G	A	AGATAATGAA ACATCTGCGA AAA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTCGTTTGGAAGACTACCATTATTCAAATTTATTATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAAA[G/A]AAGTGTGGGAATCACCTCATCGTGTGC

Name	Pos	Allele 1	Allele 2	Seq 1	Seq 2	Sequence
WI-15389a	33	G	A	AATCAACTAGCTTGCTTTTGTC	TTTGAATAATGGTAGTCTTCCAAA	AAAATTGACAAAATCAACTAGCTTGCTTTTGTC[G/A]TTTGGAAGACTACCATTATTCAAATTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAAGAAGTGTGGGAATCACCTCATCTGTGC
WI-15747	88	T	C	TGCTTCATTTTAAACTAATTTAGTGTTT	CATAATTCACCAAAAGTTCATATAATTT	TGTAATCTGCTTACAGTCCTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGTTT[T/C]TTTAAACTAATTATATGAACTTTGGTGAATTATGAACTGTACCAAAC C
WI-13752b	117	C	T	...	...	AAGAAAAGCACATACACATTTCCAGAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGCTGGATATACTTGGCTTGCAC[C/T]GGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752a	106	T	C	CCTTCTCGTTAAGTGCTGGA	CCCTCCGTAAAAGGGTGTCC	AAGAAAAGCACATACATTTCCAGAATTTTCCTTCGTTAAGTGCTGGATATAC[T/C]TGGCTTGCACCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-14339	102	T	G	CCCAATCAAACAGTACATGATTAC	TCCAGATTTCTGGAAACCG	AATCATTTAATGAATGTTCCAAACACACCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCACCCAATCAAACAGTACATGATTACT[T/G]CGGTTTCCAGAAATCTGGATAC
WI-13744	115	C	T	TGGTGCTGAACAAAACTGAA	AATCAGGAAAGATAAGCACAGC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAAACGTAATGGAACTTCATGCAGCTTTAGAT TTCCTTTGCCCAGCTAGGAGCTTGTGTGATGGTGCTGAACAAAACTGAA[C/T]GCTGTGCTTATCTTC CTGATTCT
WI-14061	68	C	T	...	...	CCTTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAGAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCATCCACCATTTGTAAAAATCTCGGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A	C	ACCCTTTCATCCATTCAGC	TGATACTTGGCAAGAGTTTAAATT	TTACAGTTGGATTAACACTACCACACTGAATTAACTATTCAACCCTTTCATCCATTCAG C[A/C]AATTAAAACTCTTGCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T	C	CTCTAAATCGATACATCCAAAACTT	GAACTGATGCTTGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACTAGATCAAACAGAAGTACCACCAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATGCTAACTCCAAAACTT[T/C]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G	T	ATTTTATTCACATTAAACTTGCACA	GTTCTTTGATATGTGGCTTAGTTTT	GGATTTTATTCACATTAAACTTGCACA[G/T]TAGCAAAAAAATCAAAAACATAAAACTAAGCCACA TATCAAAGAACAATATACAATAGAGATTTGAATTTCTCAATAGCATTGGAAGGTATTTCCATAAATA
WI-13785d	72	G	A	...	...	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACAAATGAAC AAGTGC[G/A]TAGTGACACATAAAGCTGTCACAACACAGTG
WI-13785c	56	A	C	...	...	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGAGTGTGAAGAC[A/C]CAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG

ID					Sequence
WI-13785b	40	C	G	...	TCAAAACTGCACACTATAAAAAGTGCTTAAAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13785a	27	T	C	AAAACTGCAC ACTATAAAAG TGCTT / TGTTGTGACAG CTATGTGTCAC T	TCAAAACTGCACACTATAAAAAGTGCTT[T/C]AAAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13793	88	C	G	GGATTTTACAT TCAGCCTAGAT ATAGG / GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAATAAAAATAGTTTTTACCCCCATTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCCATAAATCTATGACTTG
WI-13794	52	A	G	TTCCTCACCCT TTTCTTTCTC / AGAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAATTCCTCAATCCATTTCTTCCTCACCCTTTCTTTCT[A/G]TACAAGGTTAAGA GCCCATTCTTCAAACAAACAACAACATAGAGCAAT
WI-15729	35	A	G	CTTTGAACCAT CTCAGCTTCTT GTGTAGACTGC / GTGTAGACTGC TCTAAAGTGCC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAAGTCCCTGTTTGCAGCCCGGGCCTGCTCATTGTTA
WI-13424	66	G	A	TGAGGTTTTC ACCCTATTCTT / TTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAGTCTCCCAACTGGTTTGGAGTTTTCCCTTCTGAGGTTTTCACCCTATTCTTC[G/A] TAGACCCTGGGGAGAAAAAACACATGTGTAAGTGGCTCAGGACATGAGGGCAGGCCGTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	TCTTATAAAA GGTCAGAGGC AATT / CAAGCTGAATC TGGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATT[T/C]GAGATCCCAGATTCAGCTTGTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGTCTGCTTTAATCCTGAACATTCTTGAAGCACGAA
WI-13446	22	G	C	GCCATGTTCTT CACTCATCA / AAGGGAATCA AAATCAGAAG G	TGCCATGTCTTCTTCACTCATCA[G/C]CCTTCTGATTTGATTCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTTAGGGCCTAGTCTGTTGTTAGAAATTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	TGAGCACATA TGGGGTGCC / CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C		CAAATGTTTTATGAAGAGACTCCGAACAAACAAAATAAAGGCTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCTGTAAACAATACTAA[T/C]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C	...	CAAATGTTTTATGAAGAGACTCCGAACAAACAAAATAAAGGCTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCTGTAAACAA[T/C]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	...	CAAATGTTTTATGAAGAGACTCCGAACAAACAAAATAAAGGCTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

ID	Pos					Sequence
WI-15702a	48	G	C	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAG[G/C]GGGGTAAAGGGGGTG AGGAAAGCATGTGAGAGAAACTGTAACCCTGTAAACAATACTAATGGGTTCTTTGAACAAAATAGTTT TGA
WI-13831b	113	T	C	---	...	TTTTTTTATGGATGCACTGTTACATGTTTACATGTTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTCTCTGTAGA[T/C]GTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56	G	C	---	...	TTTTTTTATGGATGCACTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTCTCTGTGAGATGTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62	G	A	---	...	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACTAGGCCTCAGGT[G/A]C CCATTAAGCAGCATGCTGTGAATGCAAAGGAAAAGCTTAAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86	A	G	---	...	CACATTTTCAGCAACAAATCGAGGTGCAAACAGGGTTTATTTCACATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95	A	G	---	...	AGGGTGTTTTTGAGGCCTGAGGACCCCAACATGACAACGTAAGACTGTAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCTGGACGAAACCA[A/G]CACATATACAATCATCTCCCACCTCCCAACGCCTTT ACTTTCACAGCCCTCTGCA
WI-14078	61	C	T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACACATGCAAACAAGGCATGGAGGAAGACTTAGATGGTCACG
WI-14083	47	C	T	AGACTTGAGA GCTTAAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAAACACATTACTCCAGACTTGAGAGCTTAAAACAACACT[C/T]ATTTGTTATTTCACAG CTCAGTAGTTTAGAGTCCAGTAGGCTTGCCTGAGTTGTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31	A	G	CATTTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAGAAAAAC[A/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAGTGAGTGAAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAAACAGGAGGCCTTT
WI-12169	121	G	C	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAATTTATTTCCACTTATCAAGAACTTACAAATATTTTGTTTCATTTCTAAA TTTTCACCTTATTGCTAAGTTATAAAATAAAACTTCCTATTTTCTTTGCTT[G/C]TTTTTCTTCA CCTCAGAACCCCTTA
WI-15705	50	A	G	GGAGGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAATGAAGGAGGAGGAGGAGATTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTCTCTTGTACTACGGAGACCCTGCTTATAGCCCCCAACAGGAAATCCTCA TCTGCGGTTGCCAGACAG

Marker	No.	Allele	Allele	Seq A	Seq B	Sequence
WI-14379	102	C	T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTT TGAGGTTGACA	TTTATGCTGTTGTTGTTCTACTGGTCGGTCGCTCACTAATATCCAATCCTAGTATGATGATCTTT TACTTGTGTCTATTAACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGACT
WI-14102	22	C	A	...	...	TAAATAAAACAAAGCAGAAA[C/A]CCCACCATTAACAAGAGGAGACACTGCAGAGGCTTATGTACA ACACGTGTCCCGCGAGGCTGGCGGCGAGGCTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-15937	24	A	G	CGCAGAGCTG CTGTGTATTTAAAA A	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTGTATTTAAAA[A/G]ACAAGGCGTCTGGATCTCTGCAGGGGGCTGGGACCCAGCTGC AGTGGGGGCTCCGGCACTGCTCCTGCTCTCCCAGGACTCTTCCCACCACCCC
WI-15944	24	A	C	AAACTGAAAC GTATTTCCTCC A	GGCCTTTAAGT TTCTACGGTG A	TGAAACTGAAACGTATTTCCTCCA[A/C]ACACCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCCGCGGCGAAAAAGGAAGTTTCAGGTAGTACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-14124	92	A	G	...	...	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAGAGAAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14125	88	C	T	GGTTTGACCTG CATAGATTTTT	GGAATGGCATG GCCAC	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGGTTTGACCT GCATAGATTTTTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
WI-14136	120	G	A	GCTTTCTCACC ATGTCTTCACA	CTTGTTCTGTC TCTTTGGGC	GTTTATTTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCCATGGTTAGGTTCT GGTGAGGACTCTCTGCTTCACAGCTGGCTGCTTCTCCACCATGTCTTCCACAT[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14138	23	C	T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAGAAAAGCTC[C/T]TATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTTCTTTATGATTTGTTTCAATG
WI-13551	74	G	A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT	GGCCAGGTTTATTCATAATTTCAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59	C	T	...	...	TTTTTAAGAGTGTCCTTCACACTCATTTATATTGTTGCACACAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T:AT	G	TTTTAAGAGTG TCCTTCACATC TGTTGTTTTTG	TCATCTGTTCT TGTTGTTTTG A	TTTTTTAAGAGTGTCCTTCACATCCAT[T/G]TATATTGTATTGCACACAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

ID	#					Sequence
WI-14631	82	G	A	...	...	TGAATTCAAGTGGACAGTTTGCCTCTGTGTTTAGTGAAACCCTCACAAGCACTCTGCATAGTCCGCTTCTGTCTTCTTTAAC[G/A]TGCCTGGTTCCCTCTGCCCAAACTTTAGGATTGGGCCTCCTCAGGGCCTTGTCCTGA
WI-6053	24	A	G	...	...	ATCACCACCGTGTCTAAGAACAAC[A/G]TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTGCAGTACACTTCCTGCATTGAACCTGGCTTCCTGGAGGAGCCTCCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACCACGGAG
WI-15964	99	T	A	GCTCTCTGTCC CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTTCTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGGGAGGTAGTAAGCTCTCTGTCCCTGTCCCTGGAGGTA[T/A]GCAAGAGGGTGGGAGAGTCTTGGCAAG
WI-12075	103	G	A	AGCAGCTGGG GGCAC	CCCCTTCTTTC TCTTCCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAAGCAACAAAGCAGCAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGGGCACGGGGGCACGGGGGCAGCGC[G/A]GAAGGAAAGAGAAGAGAAAGGGGGAGGAGCCT
WI-12179	96	G	A	GGAGGTACGG TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTGCGTGAGGCATCTGCACATTTCCTAGAAGGACATGAATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTGCAGGGAACAG
WI-14651	49	C	G	CAAGAATCAT TCTCATTTAAA ATTGT	GGAGATATTGA TCTTTTCTGA CTTATT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAATTGT[C/G]AAATAAGTCAGAAAAAGATCAATATCTCCCCTGCTCAAAAATGACACTCCAATTTCACAGGTAACCACTGTTA
WI-14666	105	T	A	...	...	AATGTGGACTTTCAAACAAGGGTTTAAACTAATCTAATACAACTTCTACACACATTCCAGAGCATTATAACAAGAATTATTTACAGGCAGCTAATGTATTAAA[T/A]AACCATGAAAAGAAAAAACTTG
WI-13473	31	C	T	...	...	ATCTAGATGTCAGCAAATGGGCTGAGACTGTC[C/T]TTGTCTGGTAGATGCAGTGTTTATGTTTCTACTCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAATGTTTATATCACAGTC
WI-13967	103	A	C	AAAAGACTAC AGATACAAGG AAATAAAAA	TTGTGTTTTCA TCTCCTAAAAG TG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAGATAAAATATGTCATTCAGCAGTCATTTAGGAGATGAAAACACAAAAAAAAATAAAAGACTACAGATACAAGGAAATAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T	A	GCAGACACAC TATTACAGGCT G	TTAATTGTGTA AAACTCATTG TTACTTT	TTAATATTTCAGCAAAGTTATTGCAACAGGTTGAAAATGCAACAGGTTGAAAATATTAACAATTAAAATATTAACACATACTTATGGGATTTGTTGAATGA GTAACAAATGAGTTTACACAATTAAAATATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C	G	...	...	TTTTGTGTTAAGAAACAGCATTTTGAAAATAAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTAAATTTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C	T	CACCATGGCA CGTCCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACAACAACTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA[C/T]GTGATAAGTGTCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G	A	...	...	ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAAAATCATCCCCCTTTCATGATTGGAACAGTTTCCTGACCGTCTCGGGAGCGTTGAAGGGTGACCAGCACATTTGCACATGCAAAA

ID	Pos					Sequence
WI-16002	59	T	C	GATAACATAA AATGATCATG AGAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A	G	A	AAACTAAAAC CTTTGTGCCTA AAA	GTGGAATTTATTAAGCCATCAAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACTCAAGTCATCA[A/G]TTTAGGCACAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73	T	C	GCGTTTGACTT GTGCGG	TCCCACACTGC CCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTGGTTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCCAGTGTGGGACGGGGAGGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A	T	CTAGGAGGGTT GAGGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGGTGTAGATATA[T/T]CTTCCTCTCTCTC GTGGAGCCTACTGAAGACACAGGATCGCCGTTCTGTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G	A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCATTATGCTTGGCTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAGGCACACGGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTCCAGACCTC
WI-12340	18	T	C	---	---	ACACAATATAATTCCATT[T/C]CGAGTGATTGATTAAAACCTATTTGTTGTTTAGAACCAAACAAAACTAC AAGAAAAACATTTCAAAACCTTTTTTCAGGCTGA
WI-14808	52	T	A	ACCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTAAGCAACAGTTAAAAGTACCCACCACACTACCCTGT[T/A]AAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTTAGAAAACAAAGAAAACACAACTGAAGGCCCCATGTA
WI-14816	29	A	T	---	---	AGTTAAAAAAAATCGAGTCAGCATTATT[A/T]AAAAACTGGACACGCCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71	G	T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATTACAAATACGATCCATAA
WI-12542b	70	G	T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATTACAAATACGATCCATAA
WI-12542a	45	C	T	GCTATTAGGC AAACTGAACA TTTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGT[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATTACAAATACGATCCATAA
WI-12173	57	C	T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTCTAGAAACTGGGATACAGCAGTAAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCACATTCTAGAGGTGGGAAAGAGGCAATAAATA

ID	No.					Sequence
WI-14836	28	T	C	...		TCTTTGGAGGGATAGAGAGGACAGAGTGTT[T/C]GTTGATTTTCGTTGATTTTCGGTTCAGTTGGTTGTTGTTCATT GGTTTTGTTTTGCTAATTTGCCCCACCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60	A	T	TGGTGACACG GAAAATACTT AA	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCTTATGATAGCAACAACTAAATATGATGGTGACACGGAAAATACTTAATT[A/T]TTAA AGTTTGTAAAAAGTAGCAAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61	G	A	...		ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAATATTTTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACT ACCTGGC
WI-14867	46	T	C	GACATTCCAA GGCTCTCTAAC A	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCA TTCGCTTTGAGATGTGAATGTGTAACCCAGGGTGGA
WI-14733	98	G	A	CCAAATTGAC AGATATTCTGC A	GATGAGGTCAG GCCATTTATT	ACGGAGTGCGTCTCTGATGTATTCTTGTCAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAATT AGAAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAACATCA ATGTCATGAAAAAACACAAAA
WI-14898b	79	A	C	...		TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTCTCCAT[A/C]AAGCTGCCTGCTGTGCCGTTGCCTGGCTTTGCCTTAACCCCTGGTGCTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50	A	C	CATGTACAGG AAGAGTTGTCTT CCA	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGAGTTGTCTCAT[A/C]AGGTGCCACTAAGG AAAACTTCTCCATAAAGCTGCCTGCTGTGCCGTTGCCTGGGCTTTGCCTTAACCCCTGGTGCTGCATC TGCCTGTGTTCTGTCTT
WI-14907	48	G	A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTATTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCCTTGCAGCAG ACATTGTGAAGCTGCTGGTCGGCGCACACCCATCAATCAGTGACTGACTGCTGCGAGAGGGCCCACATG CACGGATGCTCACGTGTG
WI-14911	52	G	A	CCAATACATT CAGTTCCTGGT C	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCCTGGTC[G/A]AAGGTCCTTTTC CTGGTTTGCAGACAGATCCTTGCTGTATCCTCACATGGCAGAAGAGAGGAAGAAGTAATCT
WI-14913	88	C	A	...		CTGATGCTTTGACATCTGGGGCATTGTGTCTCTAGAGAGACTACTTCTCCTGGGACAGCAGCCAATTTC TAGTGATAGTAGGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCACCT
WI-14914	66	G	C	CTGGACACAG TTTTCTCTAGC A	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGTGTCGTAAAGCCTGTGAAGTCATGCACACATCTGGACACAGTTTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGGCTTGATGGCTTTCACAGC
WI-14926	49	T	C	...		GTTTATTTCAAAATGACACATCCCAGATTGAAATGGGCACTTAGCGAA[T/C]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGCAGTTTCAAATAAAAATTTCCTTAATCAGGTCCA

Marker	#			Col 1	Col 2	Col 3
WI-16083	89	C	T	ATGTTAACA CAAACATATC AAGGAT	TGGAAAAGATT CCAGCCC	GCATCTTTATTACCACAGAGAAACTCATTTATGTCCTTAATCATTGTTAATATAATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	C	T	GGAGGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCGTGTTCTGGAACAGCTCTCCTTTTCCACAGGAGGAGTCCCTCTCCTTGAT[C/T]GCGGTATTG GTTGGTTGTGGTGGATTTGGGGAGCACGAGGGAGCAA
WI-14946	47	T	C		…	TCAATACTGAAGGTGTCAAAGTGGTCTATTGCCCCCAGACATAACAT[T/C]CTCTAAAATCATCCTCTA GATCAGGGGAGTCATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGGAAAGGATT
WI-15987b	80	A	G		…	ACATTAAAACAGCACAATTAAAGGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTC[A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C	T	CACAATTAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAAACAGCACAATTAAAGGGGTCCCAA[C/T]GAGGTTGGTAGTGCTCTTCCACTATGTGAGGA CACTCAAGAAGAAGATGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T	C	AGGGAAACTG CTAACTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCCTTCAGGGAACACAGGGAAACTGCTAACTTGTCAGT[C/T]CTCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A		CAAAAAGCTA TTTTCCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCCTACACTTGAC[A/G]TAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83	A	G	AATAATTTAT CTCTTTCTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATTCAACTCTAAAATTCCAAGATGAAAAATAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCATTTCTCCAGGCCCTTGAACTGC AGCAGAAAATTCAAGGA
WI-14976	35	C	T	GTTGATTGCT TCGTTCAAAG	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTGAGGAG GGGCAGGTTGGGGGTAGGCTCAGCGGGGCATAGTGGCCACAAGAAGATGGCCCATCCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G	T	TCAGTGGTGTT TATTGGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTGTTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C	T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAAATCATGCCTACCAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACCAACTGATCGGAAAGAAACGTA
WI-15002	72	T	A		…	AAATCTCTTCTTCACACAGATGAACTTAATAAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCCT[T/A]TTCAGTTTAGGCCTCAAATGGGCTCTCCTCAAGGCTGGACCTCAAGGCCCAGTT
WI-15000	90	G	A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAAACTAGAAACAAAATCCACCT

ID	Pos			5' flank	variant	Sequence
WI-12323	68	G	A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTTGTTGATGTGTTAAATCTTATCTCTTTTTTATACACAATACTTCATGTACCTATGAAATAA[G/A]ACAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A	T	AAGGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C	A	T CCTGCCTTTAT ATTGGAATTTC	GGGAGACCATG GGTCTCT	ATTTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAATTTCCCTGCCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGGTCTCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T	A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCAT[T/A]CTCACAATACCATATACAACATACT TTCAATCACAACTCAAATATAAAAATAACCTACAAAATCACATTGC
WI-13712	40	A	C	TTTACTTTGTT GTCATTTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCTTTACTTGTTGTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTTGTTAAAATTTATGCAT
WI-16163	35	C	T	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTAAGGAGGACTATTCTTTAAACAAGACAGTGTCTGACATTTATTCAGGT
WI-13453	88	T	A	AATGCACAAA ATCTTGTCTCT TC	TCAGATTTTTA CATCTCTTCT AGCA	TTTTTATTTCATTTGAGTGCTTTATTATATATTGGGAATTGCAGTGATATTAACATTTGTACAAAT GCACAAAATCTTGTCTCTTCT[T/A]TGCTAGAAAGAGAGTGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGTCCAT
WI-16167	58	T	C	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATATAGATTTTTCTGATATACATT[T/C]CATCTT ATTCACCACGAGCACCACCACACGAGTAGAACAGTTCCACACCTGATAAATTGCACAAGATG
WI-14482	17	G	A	GCAGAACCAA TTAATAA	GA	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTAAAATCGATACTAAAGGAGAGAGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T	C			TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTCCCAGTGATCATGTAC GCACTAAAAAAAT[T/C]GTGTGCTGTGCTGCGTGGTGAGTGAACCATTGCTTAAGATAAA
WI-16156	97	A	C	TGAAGATTAA CCCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGAATACTCTATAAAACCAACCCCTTCAATA TTACACTAATGAAGATTAACCCAGAGTCGC[A/C]CTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G	T	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATATACAGCTTTTTCATTGAAGCTTT[G/T]ACCTT TACTATACTCTAGGCTATTGGGAGTGTTCCCCAC

Marker	Pos	1	2	Flank A	Flank B	Sequence
WI-15100	74	G	A	---		TCTTATTCACAGCCAAGAGAAAATACCCAATTATTTCCAAATAAAGCAAAAATTGGAACAGAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGAGCCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A	T	CCTTTATTTTC CCAAAATATAA AATTACT	GTCACCATGTT ATATTTCTT TAAGAC	TGGTACAGAATGTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAATTAAAAACCTTTATTTT CCCAAATATAAAATTACTAAATTAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T	C	---		TCTTTAATTTTATCGGAATCCAGGACACAAGAGAAAAACCCAAAAACCACATGGAGACAGAAG ACGAGACACAACTCCTCCCCCACT[T/C]GCCCTCCCTGCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68	G	A	---		TCTTTAATTTTATCGGAATCCAGGACACAACAACAGAGAAAAACCACCCAAAAACCACATGGAGACAAAG AC[G/A]AGACACAACTCCTCCCCCACTGCCCTCCCTGCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30	C	G	TCGGAATCCA GGGACACAA	TGGTTTTTGGG TGTTTTTCTT	TCTTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAAACACCCAAAAACCACCAAAAACCACATGGAGACAG AAGACGAGAGACACAACTCCTCCCCCACTCCTCCCTGCTCTAGAGTGGGGGACAAAGTGGGGGTGAGAC AG
WI-15116	96	C	T	GGGAGCCCTA GTTGCAGTAA	CCTGAATATGC AATTATTATT ATGACA	TTTTCATTTATTTTCCAGAAAAAGAAAATCACATTTCAGTAACAACTTACATATAGAATTAAACTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-12578	37	C	T	GGCCTAAAGG AATGGGAA	TCAAGGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGCCTAAAGGAATGGGAA[C/T]GTGGTGGGTTCGCTTGATACTTGGT GCTTGTGTGCATGGACAGCAGAGTCTTCCTGGTCCATGCAGGGGGCCGTCACATATTTAACTGCACTAAT TTGGGCAAACTGTCATTC
WI-15153	40	A	G	CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGTC T	ATTTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAATTACCATTTCCTAA
WI-15215	84	G	C	TGGCTTAGAA CCAACAGGGGA AAAAGTCA		CCTTTGCTCTCTGAACTGGGACCAGGATGTGAAATAATTTTGAATCTGATGCAGGTGCAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTCCCGTGTTGGTGGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C	T	CTTGAGGACCT AGAAAGCAAA C	TTTGATTGGCA TAATCACTCC	AGGAAAGAGAGTGGTAAAGCAAAGGCGATCATTGGATGGAATGATTATGTGTCACGAGCGACT.TGAGGAC CTAGAAAGCAAAC[C/T]TGGAGTGAATTATGCCAATCAAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G	A	---		AATTTGCTAGTGCAAATGGACCCAGAATTGGAAGGGCTATGTAACTACACA[G/A]TATGCCACACCAC AGCCATGTCAGTGTCACAGATCCTCTTGTGCATTCAGCTTTCTTAAAAACACATCCAAAGGCTGCA
WI-15123	55	C	T	TGTTAGTGACA GACAGATAAA C	TTGCTTAAGGG CAAACAGAC	TGACTGTATACCAAATGCTGTGTCTTAATGTTAGTGACAGACAGAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGAAGAAGAACATGCAAACAGAGATAAAAAACACAAT

ID	No.						Sequence
WI-15182	49	C	A	GCACAACCAG	GGCAAAATA	GCATGGGTAA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAACCAGGGCAAAATA[C/A]TGCTGGGATTAACCCATGCTAATGGGTACCTTACCTTTATTTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T	C	GGGCCTTGGC	ACTATG	TCCAGCA	GTGGACCTCTACAAGTACCATGGCCCTTGGCCACTATGT[T/C]CTACTCTGCCTGACGGATAAGTTGGC ATATGTTCAGATTGGTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCGACTCTT
WI-12601	42	T	C	CATTTATTGAG TATTCTTGCTT	GTTGTAGTCTT ACATGCTTACG	AGGCAGAGTAG ACATGCTTACG	ATATGTTCAGATTGGTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCGACTCTT TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTTTGATT[T/C]GTCTACGTAAGCATGTAAGACT ACAAACATTACGACCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAACATTTGTCATTCAGAT
WI-14510	104	A	T	TGGCAAAATA TGCATAACAA AA	TTGAAAAATGGT TAAACTGGCA	ATGTTGAGAGTAAATATGCCCTACATATTTAGTGTAAGTACACCCCAGATATTTTGGGGAAGAGAG TTGTTTGCTTTTGTGTGGCAAAATATGCATAACAAAAT[A/T]TGCCAGTTTAACCATTTTCAAGAGT
WI-15239	57	T	C	CATTTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATT[T/C]CCTGAG TCCAACGATAAGGTCCCGGAGGAAGGGGGCTTCCCCTCCTTTCTCGCTGGGTTGACGTTCCCAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T	C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACTGTCTAGCAGTATTA[T/C]GCTATTAGCTA TGTTTACAATTTGTCCTGAAGGGGTGTACACCCCAGAAAGTGGTGATTCCTGA
WI-15249	34	T	C	GGGCCTTGACAC AGATTTTTAAC AAAAGTTCTAA AA	GGAAAGCCAG AGATTTTTAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTT[T/C]TTGTTAAAAATCTCTGGCTTCCTGGCTGG TGAGGAGGCACAGCGTGGGGTCTTCAGGTATCCACTGGTGCCCCGCATCTGTTCCCTCCACTCCCAG CCCACATTCTTGGCTCT
WI-12159	28	C	T	AAGACACCGT GCAAATGC	CCCCTCTCCTCA GTGCACTTT	CTGTCCGGGGAAGACACCGTGCAAATGC[C/T]AAAGTGCACTGAGGAGAGGGGGAGGGTCTGTGACTC CCAAACCCTCGAATATTTATGAATCTAAGAGTCCAGACGCAGTTCATCCACGGAGATCTGC
WI-12648	41	A	G	CCTAGTGGCAT TAAGGATCC T	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAAATGCCTAGTGGCATTAAGGATCC[A/G]TAGGATGTCCCACTTTTAGTAGC AACCGATGTTAATTCACTACTCCATGTTAGGTGCTTACTTGGATTATCTCACTTAAAAACCACA
WI-12684	64	G	T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGAGGAAATTTAGCATAATTCTT
WI-15260	75	G	A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGAGGGACAAAATCAAGAATGAGCTGGAGAAATTAA TCCTG
WI-15325	39	T	C	CATGTGGCTGG GACGC	CCTTCCACCAT GATTGTGA	AAGGTTTAATGGACTCACAGTTCCATGTGGCTGGGGAGGC[T/C]TCAACAATCATGGGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAATGAGAGC
WI-13936	123	C	T	AGTTGGCATTC AATAGCCTAT C	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTCATCCATGGCATTCATGGCTTCTCACTCCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAGAACCTATGCATGGGATTAAGCCTATC[C/T]AACTCCATGT GGGAGTTTCATAATAA

ID	Pos					Sequence
WI-14528	62	T	G	TTTTAACTTTT TCTGGATGGTA GTAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAATATATATTTAACTTTTCTGGATGTGGTATAAATT[T/G]TT GAATTATAAATTTTAATTTTATATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	TATTTCTTTCGGTTTCGGATGCAAAACAAAAAAATTTTAAAGAAAATGTGACTTCAAAGGAAAGA ACAAATTT[C/T]CAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C	A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTGACATCTGGGCATTGCTGTTCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G	A	---	---	TTTATTGGCTGTCTCTGTAATACAATGTGGTGAAAAC[G/A]TCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCCAGTGTCAGGCACATAGGCTAATCAGTGG
WI-14580	100	G	A	CATTCCCATCT GTCTTGCA	CCGACCAAGAT CCCTCC	AGAATTTTTTCCTTTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAAACTTCTCAAATAC CTAGTTATTATACACATCCCATCGTCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T	C	GGCCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAAACACAGTACACCAGGCCTGCATT TGGCTTA[T/C]GTGCCTGAAAAGAAGGGCCGACCTCTTGATAAAGAATGTCT
WI-8039b	97	T	C	---		AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCACTACGCACATCGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGTA[T/C]GTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGACTAGGACAACCATGCAACACCACACCCACA GACCAGACACTCTGGGTTGAGATGATGATTTTAATGCGCAGCCGACGCCGACACCCACA
WI-8039a	87	T	C	---		AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCACTACGCACATCGAGTAAATACTG TTTGGTAAAACTTGTTCAGT[T/C]AAATATGTATGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGACTAGGACAACCATGCAACACCACACCCACA GACCAGACACTCTGGGTTGAGATGATGATTTTAATGCGCAGCCGACGCCGACACCCACA
WI-8044	107	C	A	---		CACAACATTCAGAAGTTTTTCTGCATTGTGTCTTCTCTGATGTCTCAAAAAGATTTGAGCTTTGACTAT ACGATTTCCCACACTGAACGCATTCATAAGGTTTCTCCC[C/A]AGTATGGATTCTCTGATGATTAATA AGCCCCGAATTCTGGCTAAAGGCTTTCCCACCATTCAAGACACATTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTTGCACAAGAATGGAACTTCGGCTGAATGCTTTCCCACACT
WI-8550	32	G	A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T	A	---		TATTAGATAAAAACCCTTTGTTCCCGATTCAGGATGTTTAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT[T/A]GATGGACAGCAGCAGAGGAGTGGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCCTCACAACTGCCCCCCGTCAGAGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGGTTGTTGAAGCAGCCAGATGGTAAGG

ID	Pos					Sequence
WI-6192	91	A	G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAAATTAGCTCAGTCCAACACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTTCT GACTGCTAAGGATTTAATTTGGAT[A/G]ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T	A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACTCAAATAATAAAGAAA[T/A]ATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAAATAGGAGTAAA CATATGCTGCTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTCTAACCACTCCTACAAGAAGTTAGTATGTATTGTCATTACATGTTT ACTTTTGATATTGTCTCATTATACTATGT[C/T]TATATAATAATGTAGAATACAGTAGGTAGGTGATCC TGCATTTCAGGTAAGCGGTAGGTGGAAATCCAGATTTCCTCTTGAGGAAAA
WI-6213	164	C	T	---	---	CGGGTTAAGAAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGGCTGTCATCTGTGGTG TCAGTCCTTCTGGCCCCCTGGCTGTCAGTGTCGCTCCAGGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCCACCATGGCCCTAGGGTCGTCCAACAAGTCCAGCAATCATGGCGTTCTCGTATCTGATCC AC
WI-6217	131	C	T	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTTTGTTTTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTACAGCCTTGTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTTGAGAAAAAACTTCTCAAAATT[G/A]GTTCCAGACTTCAGGAAAAATGATT TCCACACATGGGTAAGGCCAGAGTCTCCAGTGTTGGTCATCCAGAAGCAGCTTG
WI-6238	175	G	A	---	---	CTTGATTAATCAGGGCTTTGGGGGTCATAGGGGGGATTAGTCACTGCACAGTCATAATAATGCATTTA TTCAGGGAAAAACTTTAAT[C/T]TTCTTTGTCTTGAAACTTGATTCCTTGGGCCAGAGGAAGGTCTTTACTGTAG GGGATGTTCATCTAAAACACCTTTACTGAAACTTGCCAATAAATGAATACTTCATACAGGCAAGAA
WI-6272	86	C	T	GCATTTATTCA GGGAAAAACTT TAA	CTGTTTTTGGA GAAGACAAAG AA	CAGAGGACTTAATGCCTATTCGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA[G/A]CTGCAAAGCCATGGCTGCAGACATCAGGAGAAGCT TCCCAGCATCCCAGAGAAGCTCTGTCTGCGGTGCAGTTCAGTTCTCGCCTCCGATTTCCTGCCAGCAGTCTTCCTCTCTCATTCTTCTCTGGCCCC
WI-6303	96	G	A	CCCAGAGAAG CTCTGTCTGC	CAGCCCATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAAGCCCAGCGTGTCATGCATCCTGCCAATCAATCACTGTATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGTGT[C/T]CTGGTT CTTCCCTTTACATTCTTTTGGGGGA
WI-6315b	193	C	T	---	---	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAAGCCCAGCGTGTCATGCATCCTGCCAATCAATCACTGTATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAG[T/C]AGTGTCCTGGTT CTTCCCTTTACATTCTTTTGGGGGA
WI-6315	187	T	C	---	---	

ID	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-6375	28	A	G	GGTTATTGCA TATGGAAATC AA	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAG[A/G]TATCTTTACAAAAAAAGGTTAGAATAAAGATCTCACATTTGTAAAGGCACATATGAAACATTTATAGCAAGCACAAGGCAGTGAGACATCAACAA
WI-6409b	112	T	A	...	...	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAATTCAAACATACAAATCAATTACAACAAATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAGGACACCAAGAGACAATAGGGCT
WI-6409a	73	A	T	...	...	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAATTCAAACATACAAATCAATTACAAC[A/T]ATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAATGCAACTGACAGTTTTGAAGGACACCAAGAGACAATAGGGCT
WI-6523	165	G	T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAAGGTTGATA CAGC	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGAGATTTTGCAGCAGATTTCATTATAGTTACTTAACAGCTAAATAAAGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGAGGGGGAAAGGAAACAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG
WI-6554	195	C	G	...	...	TCTCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGCTCCTGGAGTCCAAACAGGATGTGGACGTCCCTGTAGTTCTCTCTTTCACACAACTTTTCCCTGAGAACTGTCCCAGTGCAGGTGGACCTTCACACAACGAACAGCTAAACTCTGAGAGAAAAAC[C/G]CTGACTTTCAGAGAAGCATAAAGCTAAAGCTGAGAAAA
WI-6558b	68	C	T	...	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTCCCACTTTGTTTTAAA[C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTGAAAAATGGGCG
WI-6558a	42	G	C	...	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATT[G/C]TGTAATGTTCCACTTTGTTTTAAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTGAAAAATGGGCG
WI-6629	75	T	C	TCTTTTCAGAG AATAAAAGTT GTCATA	TGACACAGCAT CCATTGCT	AACCAAACAAAACTAAGAGAAATGGGAAAAAGAAAATGGCAGGTGAAGAACTCTTTTCAGAGAATAAA[T/C]AGCAATGGATGCTGTGTCAGAAACATACTGCCAATAAACTTTAAGAGAAAAAGGAAGTTGTCATA[T/C]ACTCAATGAAGTTACTGTTGTTATATAAAACAGGAGCTCACAGAAGAGTTAAGAGTTAATGGAAGAT
WI-6644	134	T	C	...	...	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAAATCAATCAAAACTCAAGCTGTTTCTCTGTCTTTTTACTTAGCAAAGGAAAACTTAGTGAATGCTACTTGACAAGAAGAAAGTCATTTCTCAAGCACA[T/C]ACCCAAACTTGAAGGTGATTGAACCCAAATAATGGGTGGGAAACACCAAATGAGGTGGAGGAATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6690b	106	C	T	CAGACTCTGG AGCCACAGC	ACATAAAAATA TTGCAGTGTAT TAGCC	TGCTAAAACACCACCATTATTAAGGAGAGTACTAGGAAAAAACTACCAAACACCAGCATGTGAAACAGTTGGGCACGGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]TGGCTAATAACACTGCAATATTTATGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGCGGTATCTGG

ID	Pos	A1	A2	Seq 1	Seq 2	Sequence
WI-6690a	28	T	C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTTGG TAGTTTTTCCT	TGCTAAACACCACCATTATTAAGGAGAG[T/C]ACTAGGAAAAACTACCAAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGCACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGCGGTATCTGG
WI-6770	53	A	G	CAAACCCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAAACCCCAAAACATCACA[A/G]AATTATTCAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A	G	GCATTCTTCCA AAAACAAAGA A	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAATGTTCAGCAAATCAGCTAGCACTAATCTTGACCAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTAATTTAGATGAAATTCACATTTAAAAACATGGTAACTCCAAGCATTCT TCCAAAACAAAGAA[A/G]AACATTGGAATAGTCACTTACACAAGGAC
WI-6761	32	C	A	GATCTAACAG CTGCAGAATG G	AAAAGCTGGG AGGGAAGAAG	CCTGAGAGGCAGATCTCAACAGCTGCAGAATGG[C/A]CTTCTTCCTTCCCAGCTTTTGTGAACAAAAC AATTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTTGTTCAGGTACAAGGTCTC
WI-6844	225	T	C	---	---	TAAAATACTGCCAACTAGCATTAGTGTCCACTCTTGCATCATTAAAAACAAAGGGTATTCCTCCTTG GTATTTCAAATGATGCATTATACAATAAACGAAGTTAGAACTTAAAATGCACCCTGATTAATTATG TAAACTGGTAATTTGTTTAAAAAGCATAATAATTGGTTCCTTTCTTCATAAAATGGAAATTTAAA TATTTCTTCTGATAGTCTT[T/C]GAGGTTTTTTAAGGATTTTTTCAGGTCTTGTCAGCAACATCAA
WI-6824	112	A	G	---	---	CGGTTTTGCTACACTTTAATGGGTTTTTTAAGGATTTTTTCAGGTCTTGTCAGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGCTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCCTCCTTCTTGAGAGCTTACAGTGTCTAGGGATTGACAACTCACAGT CTTAGGAACTGGGCAAAGTAAGGCAAATTCTTCATCCCCTAGAGCTATTGTG
WI-6889	139	T	C	GAAAAATGAG ATGCAGTTAA AATTC	TCACTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCAACATGGAAGTGTCAAGAAAACATTCGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]AGAATAATTAAAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTTGTAGATT CTCT
WI-6911	216	T	C	---	---	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGCACTCAAATATCTGATGAACTTGATGAACTGAA AAGAGGTCTCTTAAACAAGATATCATCTCCCGAAGAGAGAAGTCCCAACCATATAAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCTTCCCCAAGGAATGTGTTTCTAATTTGGTTTCAAAGCACACTGGTTCC CACTTTACCACTT[T/C]CATGACATTGGACAATAGTACTCTTTCTAC
WI-9413	112	G	C	---	---	GCCAGTCTCTAGTAAGTCTCTAGGACATGACCAGGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACTTGGGTGGAGGGATACCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74	C	T	---	---	AAAAGCTTTAAAAAAAAAAGTGGTGCTATCTTTAGAAACACTTTCAGCAAGATCAAGAGTCAAGAGTAGCCCAGCT ACAGCCCTC[C/T]TGGTGCATCTAACCCCTCCTTTT

Marker	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-9617	37	G	T	--	--	TGCTCTTTTATTTCACGTTTCACAACACACGCCGTG[G/T]TGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGGCCGGAAGGTCTCATTCTTGCGTCTCTCTATGGAGACTGATTGAATTGGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCCACTCTGTGGGCAGAGAGGCTGAGCCCCTGCCCACACTGGCCACCA AAGAGGTTGCACGATGCCAGCTTGCAGTGGGGTCCAAGCCGGGTGTGCTGTG
WI-9657	121	T	G	--	--	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAG[T/G]ATAATTCTT TGTATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G	C	AAAAATTAAC CCTCCCAAGTA GCTGGGA	CAGGTGTGGTG T	CAGGGTCTTGCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCACATGT[G/C]ACACCACCACTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51	C	G	--	--	CAGGGTCTTGCTGTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACT[C/G]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGCCACCACCACTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCCGTCTCAAAAAACAAACCAACTAA C
WI-13112	71	C	T	TCATAAAGAC TACAGACTTA AGCTTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTTATGTGTAGAGTCACATACTATTTTATTGAGGGAATAGGCCAAT TT
WI-12988	36	C	A	TGGTACGTGCT CTACTGATGCT CTCAGTACAA	CAAAGTGTACA GTTT	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[C/A]AAAACAGCAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTAGCTTAGTAGAAAAGAAAGCCCAAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTCCCCTGTGGGATGAGATGTATGCACACAAGT AAA
WI-13020a	108	G	A	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCCTTTGCGAGA GTTT	TGCTATTCATGACAGACACGTGAGACAAATATTCTTATTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAACCCTGAGACTTTA[G/A]ATCTGCAAAGGGGTTTAATAAT GCAAATATCACATATTTCCATTTTAACACCATATTTAAGTTTCCATTTCTTAATAGAAAATGA TAAAAAATGTTTTCCCCAATAT
WI-12837	87	A	G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTTT AGTTGTGTCCA	TGTATAAAAATCCAACTTGTTCCACAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[A/G]TACAAAAAAAACAGCATTTCCTATGGCCAGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAATGAGATTGCACACTAAGGCAGGAGCAGGAGAAGCA

L42611b	50	G	C		...	GTCCTCAGGGCCCTTCTCTGGCTGCGAGAGCCGTCTTCTCAGGTTGCCTGCTGTC[G/C]TCTCCTGGCCTCTAG TCTTCCCTGCTCTCGGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGTCTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCCATCGAGATCCAGATCAAACCTTGATTTACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
L42611	34	T	C		...	GTCCTCAGGGCCCTTCTCTGGCTGCGAGAGCCGTCT[T/C]CTCAGGTTGCCTGTGTCTCCTGGCCTCTAG TCTTCCCTGCTCTCGGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCCATCGAGATCCAGATCAAACCTTGATTTACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	179	C	T	A	TGAAGAAATG GCTGATACCA / ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAAAATCAATTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C	A		...	TGAACGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAAATCAATTAAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGAAAGA[G/C]AAGAAAAAAAGAGTCTAAATATTCAG CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G	C	A	GCAGATTGGA AGTGTGAAAA / CACTTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAATGAAAGA[G/C]AAGAAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGCTGCCCTCAACTGTCTTCTTACCCACTTAATCTGCAATTTGAAAACTAGATTGAAT TCCTTTGCAAAACCCTTGCATCATGGATACCGAGTTAAACCGTTAATTAAAAGACATTAAACATGG CCTGGGTG
WI-1231b	141	G	A		...	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCTCCTTCTTTCATTAATTTTCTT TCAC[G/A]TTATTCCCTGAACGCCCTTCCTTCGTAGTGACATTTAAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T	C	A	GGCTCTTTATT CTCCTTCTTTC / CGTTCAGGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCTCCTTCTTTCAT[T/C]TAATTTT CTTCACGTTATTCCCTGAACGCCCTTCCTTCGTAGTGACATTTAAAATCCACTTTACA CATTCGGACC
WI-472	114	G	C	A	ACATACATAT CCATTATACA / GACCTTTCTT TCCAGCCC	GAAGGCAGGACTGTGTTTTGGAGGACAAAAAGTAAAATCTTTTATATCTTTATTTTATTTTATT TTTTCAGGCATATAGACATAGACATATCCATTATACAACAGAAAAG[G/C]GGGCTGGAAAAGAAAG GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTGGGCTTGATT

WI-478	46	C	T	GCATGTCTGTG TTACTCTATTT TGTTC		AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTGTTC[C/T]AGCCACCTGTGGCATTC CAAAATATGATAATCTCTGCCACCATACTGCTTAAACACAATAGAATCTGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTAAAAATAAAAACCAAC ACTGCCCA
WI-533	29	T	C	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTCTAACT[T/C]ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCTGTCCAGTTAATCCA
WI-601b	112	T	A	...		TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGAGGTTCATTGACTCCTAAACTGAGTACT[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C	T	...		TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAGAGAGGTTCATTGACTCCTAAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGCAGGTGCTGAGTACAGGAT
WI-863	107	A	G	CTCCCTTCACAA CCCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCGCTTCTTCTTCACCAGTCCACAACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCCATAAA GCCAAAGCCATTTAGTCTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G	A	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCC[G/A]GCTGTCATGTGGGATTAGAATAAAATA AACACAAAAATGAAAACACACGATTCTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37	A	T	...		TGCATTCATTATGCACCAAATAATAACTTCTGTACATA[A/T]CATTATTGTATTTCATTATCACAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACCTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACACTGACTCCTTTTCTCCTTGAAAACAAGGC
WI-1011	70	G	C	CAGTATCTGA AGTTTTTGTCT CCCA	AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTTGCAGTGGATACTGTTTTTGAAGGCTGTCGTCTCAGTATCTGAAGTTTTTGTCTCC A[G/C]AGAAGTCATTTTGTAGGTGTTCCTGGGCGTTTTGCTACGTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCCTTGCAGAGCATTATCAGATGGCTGTTTGCTGCATTCTGTGCACTGAAG
WI-5381	178	A	T	...		TTCATGCAGAAGGTCCATGAGTTTACAGAATCTCAAGGAAGAAAGGCCCCTAGAGATGACACCAGAA ATGAGAGTGGGCTTGCTCATGAAATTGGACAGACATGTTCCAAGGAACAACATGGCAATTAGTTTTGT[A/T]TTACTAAAACACAAATGT AAAATCATACTCTATCCCACGTGCAGAAACAAGGATATGTTGGCAAATGGTATTTCTGTGATG TTAACTTGGGGGTCCACAAACAAGGATATGTTGGCAAATGGTATTTCTGTGATG
WI-5791b	76	G	A	...		CTATGTATTCCATCTAGCAAAAGCAAAAGCAAGACTATTTGGATAAGTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G/A]ATCGAAAGAAGGAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTAAAGAAGAACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTTGT TAGGAA

Name	No.					Sequence
WI-5791a	44	C	G		---	CTATGTGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAAGTTT[C/G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTCATCTAGTCCATAGACCCTATCCTTATTTGCCACCCTGTTTGT AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTCAGATTTGCATTTCTTATTTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C	T		---	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC[C/T]TATGAGCCCAC ACTTCTCATTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGGCAA GG
WI-5406b	118	C	A	AATGAGAAGT GTGGGCTCAT A	CCAGGATGTC AAGGTGAGAA A	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAA[C/A]CCTATGAGCCCAC ACTTCTCATTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGGCAA GG
WI-5406a	42	A	G		---	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAGGAAGAAAAAGAGAGGCAA ACTTCTCATTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGGCAA GG
WI-5798	48	G	C	ACTGTTAGAAA ACCAGTATTT TCAAT	TTTATTCTCCC TTGTTTTCTT TG	CCATTCCTTCTCCCTCCCTCCCTTATTCTCCCTGTTTCTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATACTATTGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T	A	GGACTAATTCA TGATCCGATCT	TCTTCATGAAT TCATCTTCAG TTT	CCTGCTAATAATAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[T/A]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C	T	AGTTTCTAAAC ACAAAATATG GTTTAAG	TCCCAGAGAA AAATCCAAGA G	TGTTTAACCCAGGCAGACCTCCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTTGTGTTTA GAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A	G	TTACTTCCAGG CTCCAAGTATT	TGTCATTTATG CTGCCAGTCG	AAGCCAATTCACATTAGTTGATGAATTTTACAGTATCTAATGCATGGGCATCTGTTTC TCTGTTTTTCAAGAGGTAGTATTGTCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACTGGCTATTTCACAATTA
WI-5481a	29	G	A	CCCATGCATTA GATACTGTAAA ATT	CCAATTTCAC ATTAGTTGATG AATTT	AAGCCAATTTCACATTAGTTGATGAATTT[G/A]AATTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTGGCTATTTCACAATTA
WI-5492	38	T	C		---	TCATGAGTCTTCTTCAAGATCTTGTTAAAGTCCCA[T/C]CAAAGAAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTAGGATATTTTGCAGACCAA

Clone	Pos					Sequence
WI-5826	134	T	C	---		TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTCTATTCATGCTTCACATTTATTTTTTTTCACTTAGTTAAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAG[T/C]TTCAAATTAAATGCCACCACCATAGAATAATTTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTTCCTTGGTGCATTACTCTTTACAC
WI-5546	40	C	T	CCCAATACTTT TTCAGGTGAA A	CCTGTATTTTA GCAAACATGGG	CCTATAACCCAATACTTTTCAGGTGAAAAAAGGGAAAA[C/T]ACCCATGTTTGCTAAAATACAGGAGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTCTGATGTGGGAAATATTAGAAAATTAAGCGAGAGAGGCA
WI-5552	97	C	T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCCAGG	TGTTTGTTCTGCACCTCCCCAACAAGTGGTCAATGAGCCTCAAGGGGTTTGATTGAGCGGGGGTATGGGTGGGGCTATCGGCACCAGCCCTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACTAGTGTCAGA
WI-5836b	161	C	T	---		TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAATAAAGATAATAGTATCTAAAAAAAAGAGAGAGAATTAAAAGTGGATAGACATGAAGTAACTCTGATGATACTGGTTGTATCCTGAATCCTGCAAATATACACATGATTCAATGATC[C/T]CCATTTTGAAAATTAAGCTTTTGAATTGTTTTCCAATG
WI-5573	58	C	T	GTTCATAAGG AGGTGGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCACCCTGATGATGATGGGCGTTCATAAGGAGGTGGGGA[C/T]GACACATTACTCTCCAACTGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G	A	---		CAGGACCTTGGAGCCTTTGCTGTTGTCCTTCCACCCTCACTCTTCTCTGCCTGCCCATGGGTGGAGCCTCTCTCAGGCTTCCTCTATGCAGCCGGTCTATCTTCTATATGGGCAATATCCAATTGCC[G/A]TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5850a	92	C	T	---		CAGGACCTTGGAGCCTTTGCTGTTGTCCTTCCACCCTCACTCTTCTCTGCCTGCCCATGGGTGGAGCCTCTCTCAGGCTTCCTCTCATGCA[C/T]GCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCGTTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5612b	125	A	T	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCTGATTGACACAATAGTTATCTGACAGTAAATCATTCTAACATCACAAATATCTTATTTCTGCCTGTCACACTAATTTGCAAAGCATTCAATTGACTATTAATGAGCATCGTGTCATTC[A/T]CAGTGTTTTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5612a	44	T	A	---		TGCCTGATTGACACTAATAGTTATCTGACAGTAAATCATTCTAACA[T/A]CACAAATATCTTATTTCTGCCTGTCACACTAATTTGCAAAGCATTCAATTGACTATTAATGAGCATCGTGTCATTCACAGTGTTTTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5636	26	A	C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCAATTTTATCCGCAATAAA[A/C]TTCCCAAAGTCCTCGATGGAGGCATTTCAGAATCGGGGCAGGGGAGGCAGGAAGGTGAGAAGGTGAGACAGATGTGAAGAAC

Name	Pos	A	B	Flanking 1	Flanking 2	Sequence
WI-5865c	103	C	G	...	...	TTAGAAACCTCCATTTATTCTGCCATGGTACACATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCAGCCTCTATCAAAAATTAAA[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAGAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
WI-5865b	99	T	A	...	...	TTAGAAACCTCCATTTATTCTGCCATGGTACACATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCAGCCTCTATCAAAAAT[T/A]AAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAGAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
WI-5865	165	T	A	...	...	TTAGAAACCTCCATTTATTCTGCCATGGTACACATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCAGCCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[T/A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCTTC AGAGAAGACAGACAACTAAATAAATTCCAGG
WI-5874	76	T	G	CATAGCATGG ATAATATTAT ACAGAAAAAA	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTCATTAGTTGTTAATTTTGTGTATTCATAGCATGGATAATATTATACAGAA AAAAATT[T/G]TACATATCAAATGACTGAAACTTACTAGGTAGCAATTGTTTGTCAATTTGCT
WI-5752	36	A	T	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	CATGGGAGCCGACGTTCAGCCTCTCAGTTTTTCCATC[A/T]TTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATTGCTGATGGTAGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
WI-5760b	61	C	G	...	...	TTAGCAGAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTTCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTCACACA GTTGTCTGTGTTTAAACCTCTGTTTTCCGATTTTCCGATAAATACCAT CATTGTTGAAAACGAAGCCACGTTTTCCGATTTCCGATTAGTGTCTGTT
WI-5760	187	G	A	...	...	TTAGCAGAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTTCCGATAAATACCAT TAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTCACACAGTT GTCTGTTTAACCTCTGTTTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCCGATTCACACAGTTAGTGTCTGTT
WI-5944	52	A	G	TTCTCACCATG GGAATCTTG	GGGTGGGGATCT AACTTGCA	AATATCTGGCCTTTTCTTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCCTCACTATTGAGAAGCTAAAAGTGAAGACTACTCATTCTCAGTCTTCCTTGCTG
WI-5967b	148	C	T	...		GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTCCAATCACCCATTCCACTTATTTCCTATTAT TAATGCTTGGTA[C/T]TTGCTCTGTGTGCCGATCGTGTCGCTCCAATCACCCATTCCACTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG

ID	Pos			5' flank	Sequence
WI-5967	165	C	T	---	GAGTTTAATGAATCCTGTGTTCCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTCAGCAGCAGATATT CTTTCATGGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTAT[C/T]GCTCCAATCACCCATTCCACTTTATTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	G	C	---	GGGTAAGATCCAGAGCCACCAGGTGAACTCGCCGGTATTGAAGTCTTTGGGGCCA[G/C]GTCTGTAATG ATCTGACTTCTCCCAGAACCCCCTCTTCTCTGGAAGTTCCAACTGTCCAACCTTGAGCCCATTGTAGGGGA GCATTTGAACCCAAAACCCAGCGACACTGCTGACTTCAGCAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T	C	CTTCTTAATTA AGCATCTACA AGGTACTT / TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAAAATTGAATAATTATTAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTA[T/C]CACTGTTCTGTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAATT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45	T	G	CCAATGACTT ATTCTATATCT TGTGTCACA / TTGTTTGAAAT GTGTGGTACTT CT	ATAGGACAGTTTTCTTCCAATGACTTATTCTATATCTTGTCACA[T/G]AGAAGTACCACACATTCA AACAAGAGCCAGGTATGCCCAGGTGGGATTATTTCACGGTCAGTGTAATATGCATGTAAGACTA TTTTTACTGGCCTTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88	C	T	---	CAGTTGTCATGTCCCCTGGTACTAGAATATAGTCTTTATAGAATATGTGGTTAGAATAAAGCCACA AATTATTCTATAAAAACAACA[C/T]AAGGAACGAGGCTCAAAGTGGAACAAAACGGCCTTAGTTTC TAAGTGGAAGACTAAGACGATATAGGAAAATATATCCGTGACCTCTTA
WI-7466c	141	G	A	TTTTCACAGTC AGTCGGCATGCC AATTTATAATT / TTTGTCCTGG	GAAACTATCCTTAGTGGTGGTGCCCACATTTCTATTTCTATTTCTGATTCTTGGTCACACAGGGGACTTTCTGGGCT ATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTGT CCTGG[G/A]AATATCTCACAAATTAATTATAAATTGGCATGCGACTTTCTGATTAGCCTGACAGG ATTGTTCCTTT
WI-7466b	80	T	C	GACTTTCTGGG TGTCTTTATG ACTGAA / CTATGAAATA ATAACTAGTTC	GAAACTATCCTTAGTGGTGGTGCCCACATTTCTATTTCTGATTCTTGGTCACACAGGGGACTTTCTGGGCT ATGAAATAGTC[T/C]ATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTT TGTCCTGGGAATATCTCACAAATTAATTATAAATTGGCATGCGACTTTCTGATTAGCCTGACAGGA TTGTTCCTTT
WI-9814	104	C	A	---	TGCTTTTTAAAAAATAACAATGACCACCACCTGACACCATAGTCGTGTCTCCATTGCCACGTCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT[C/A]TTCCTTCAGAAGAGCACTTGGCCCCT CATAGGCATTCCATAGATATTTGTTGAATGAATGTGCTTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55	A	G	---	CCTCTAACAAGAAGAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTAATAATTT[A/G]AGTAACCA AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC

WI-9720a	47	A G	...	CCTCTAACAAGAAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCT[A/G]ATAATTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	...	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGTCTGCGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGCT[A/T]GAGGATTAG TAAGATCTCTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTCACCAGGGTTTAGTTTGCATT TAAGAATTGCCAGTCTTTTGTCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	...	CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTTCTAATTTTTATATGTTTACCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTTCCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTATATTCCCCA
WI-9943	91	T C	...	TGAGGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAGCAATTCAATGTTGTGGGCACTGTT CGTTGTGTTTTATATCCATCTTC[T/C]ATTTTAATTTCTACTGAGCAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTAATATTGCATTCACACCTTCTCTTTTTGTCATTTAGGGA AGGGGGCCTTCACAGATCCGTCAGCTCAACACTGCCTCCTT[T/C]AGTGAGCCTGTGAACCACCCAAGAC GGCTGGTCATCAGTGTCATCCTTCCTTTCCGGACAACTATCTTTAATAAATCCTTATTAGGCCAAATCCAAT CTTTGAATGTATCCATTTTATCCCCAAATAATCTTGTTTAATAAATTCCTTATTAGGCCAAAGGGATTTGCAA GTGCTGAAATATCTGCCAAGCATGTCATTCTACACAAAAGGGATTTGCAAA
WI-9891	39	T C	...	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTTGTTCTCAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGTA[C/T]AAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897b	84	C T	...	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTTGTTCTCAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGT[A/T]CAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	...	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGGGAGTTCAGACA[C/A]AGCCAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935b	115	C A	...	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTTGCA[C/T]ACCTCACCAGAACTGGAAGG AGTCGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGGGAGTTCAGCAGCAGCCAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935a	42	C T	...	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCCATTCCTTTGTCTTGA TTCCCCAAACCCAAGGTTCTCACCCAATCTGATCAAATGCTAACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[C/T]AGACACAAAGACAAAGAGGTAAAGTTGCTGTCTCCTCAAGAGAGAGACATAA
WI-9983	146	C T	...	AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTTGCGAGGGTGAGCAAGG

ID	Pos	A1	A2			
WI-10019	139	A	T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGCTTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAT CTA[A/T]TCCCCTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T	A	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAATAGCAGTGTTTTATTGGCGAGAAAGAAATCATGACTTTTT[T/A]AAAAATACC AGACTAATGATTAAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGCCCT CCTTAGA
WI-10020a	39	T	C	TGTCATCTTGA CTCGTATTAA ATAAAATT	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTA[T/C]GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAATAGCAGTGTTTTATTGGCGAGAAAGAAATCATGACTTTTTAAAAATACC AGACTAATGATTAAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGCCCT CCTTAGA
WI-10064b	170	C	T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	GTAGCAGGAT CAGGGAAGG	GAGATGCTG CAATTATAT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCATCTCTCTCCATGCACCAGATATTGTGGTGACACTCTGTTTAATCCAGTA TCCCTACTCCTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	TCTCCTGTCCC CAAACTCTT	ATTCTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAAACTCTTA[T/C]TTAATTCCATTCAATACAACAAGAATTTATAGAA TATGCACCACATGCCACAAAGACACCCTTATATTAGT
WI-1319	40	A	T	TGGCACTTAG AACATAGTTT ATTCTT	GCCACACACC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTT[A/T]ACCATAGGGGTGTGTGGCTTATCT TTACCTGGCATGGTCCTTAGGTCCTGTGTTTATAATTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACACTGGTCAGATGTGTTAAAACTTGTTGAACCTGCAGC
WI-10316	104	T	C	CTGTTGATTTT CTACCTCTATT ATTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTCTACCTCTTA[T/C]TAAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGGTCCAGTATGAAAGGATGTTTAAAAGCCCAGCC
WI-2572	61	C	T	...	...	AGTGAGTTGTGCACAATTTTGGAGACATTCTGTGACCCCAACTTAAAACACTTCTCCCCACA[C/T]AC AAAGTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

Marker	Position	Allele 1	Allele 2	Sequence A	Sequence B	Flanking sequence
WI-10368	31	C	T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAACTGCCTGAAGCAACCAGGTCTTGTT[C/T]CTACCCGTCTTAGAGAATAAATATATCTT GAGATAGGGAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTTGTTCTACCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTCAGGG T
WI-10391	32	A	G	CTGTCTCAGGT ATGACTCCCA GA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCCAGGGGACGCATCTGACACAGCCTTTGCTTGCTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A	C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGGATGAAATTATATGTATGCCTGACTTAGCGGGTGCTCAATAAATATTATTCTTTTTCATATT TTCCAATTATTAATACTAGAATTTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAA[A/C]AGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-10567b	82	A	C	...	...	AGCGGATGAAATTTATATGTATGCCTGACTTAGCGGGTGCTCAATAAATATTATTCTTTTTCATATT TTCCAATTATTAAT[A/C]CTAGAATTTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-10567a	60	T	C	GGGTGCTCAAT AAATATTATT CTTTT	AAAATTCTGTT GGTGAAAATTC TAG	AGCGGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATATTATTCTTTT[T/C]TCAT ATTTTCCAATTATTAATACTAGAATTTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-11153b	84	C	G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCT C	CGTTGGGAATATTCTCTATCTCACCTAAATTATGCGTGATTAAAATATACATTTAACAAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTTGGATTTTGAGTTTTTCTTATTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33	C	A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTGAAG TTTGTTAAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTATG[C/A]GTGATTAAAATATACATTTAACAAACTTC AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTTGAGTTTTTCTTATTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCT TATGTATT
WI-2616	125	T	C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAACCACGCTTAAATCACAAATCACTTTTCTTTCCTGTA GAGCTCAAACTCAGTCTGAATGAAATTGCTGCACAAATGTAACAAGAGAATTGATCCTA[T/C]ACTGGG ACTACAGCCATGGAGAAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C	T	CAAGTGAATT ATGACCAAAA TGAGA	TGTCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACAGCACACACAAAAAGTTTCACCAAGTGAATTATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAAACCTCAAATGAAATGAAGAGACAAAATATAGTTCAAAGATTCAGGTTCAATATTTGT
WI-10656	59	T	G	----	----	ACCTACAAAATAGGGATAGTCATGGTGTTGGCAGACTTTCTTTCCTTTTCTTTTTGT[T/G]CTCTTA GAATCCATTTTGCTTTTGGCCAGCATTCCCTCTCCCCATATTTAAGGAGAGAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGCAGTTACTATTCACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC

Marker	Pos						Sequence
WI-11169b	154	T	G	TTTTT	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAAAATTTAAGCCTAAAGTAGTAGTGCTTTTAAGCCAAGAGAGTTTTCATTCTTTTT TTTATCATGTGTTCTGATAATTTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A	G	TTGAAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAAAATTTAAGCCT[A/G]AAGTAGTGCTTTTAACCAAGAGTTTTCATTCTT TTTTTTAAAAAGAGCAGACATTTATCATGTGTTCTGATAATTTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A	G	---		---	CAAGTGCTTGGACCTTGGATAGGTC[A/G]ACGGCTGAAGGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCCTTTGGGTTACCACTAGGGGTCACTAAAG AGAGATGGGAGGACAGTCCAATCTGTCTAAATAATTCCAAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGTCTCTCTAACTTTAATGGGCATA
WI-10686	133	C	T	AAGG	TGCCCCTGTCC TTCATGTGTAG ACACA	CAATCTCTAAA	AATAACCTGTGGCACATAAGGCAAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAGATGATAGTTCTGCTAGAAATCTTGAAATCTGATGCCCCTGTCCAAGG[C/T]TGTGTCTCACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T	A	A	AAAATGATTCTT CTGTTCTCACA TCTGCTCAAAG TTCTTTTTGAA AA		GGTAGGATGATTCTAGAATGCCACTTACAGCCACTGAAATATATTGCCTCCCAAATGATTCTTCTG CTCAAAGAG[T/A]TTTTTAAGTTATCTACTTATTTATATTCTGCTTTTTCAAAAAGAATGTGAGA ACAGTACAAAATGTGTTCAGTATAGCAAATTAAAATTAATTAAAAAGTAAGAAAGAAGCCAATT TGGGC
WI-10694	144	A	G	TATGAGTTTTC	TGCAAATGCTT GGCATTTGTA AAGGAGGAAA	TCTCTTTTCTC	TAGAGAGGGTCTTCAGTTCAGGGTTGGAGGGGTGGTGTGAGGTCTGAGGAAGAACTCAGTTCAAATGTCTTTA TATGTGACAGAAAGATAAACTCTGAGAAGAACTCTGAGTCTTTGCAAATGCTTTA TGAGTTTTC[A/G]TTTCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAGCTTTCT T
WI-2716	23	T	C	C	TGAATTCATCC AGAAAAAACAG	TCTCTTTTCTC TTC	GTGAATTCATCCAGAAAAAACAGC[T/C]GAATGACAACAAGAGAGAAAAGAGAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCCAGTGCATGGAGCAGTG
WI-10719	115	T	C	AGCC	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC	CAGGCCCAACTCTGTCATTAAGTGTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTTGTATGT GCCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAG[T/C]GGCTGCTGGCAGTGCTT TTCCAGCCTGCCCATAACTAA
WI-10721	40	A	G	CTCA	TGGCTCTGCTA CTTGCCA	GAAACTCCCAC ATAAATAAAT	CAACCAATTCAGATTTAATTTTTGGCTCTGCTACTTGCCA[A/G]ATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAAATAGTATTCCTCTTCCCTGCTTAGGTTTGCTTAGGTTGAAGAAGTTGAA

WI-11204b	88	T	C	---	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGAGTTGAGGTAAAAAGGGGTG AAAAGAAAAACTTTCACCTTT[T/C]ATTTAAAGTAACATAAAGGTATTATGTACATTTAAGTGAT CAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAG GCAACATC.
WI-11204a	80	T	A	GTAAAAAGGGG TGAAAAGAAA AACTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGAGTTGAGGTAAAAAGGGGTG AAAAGAAAAACTTTAATTTATTTAAAGTAACATAAAGGTATTATGTACATTTAAGTGAT CAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAG GCAACATC.
WI-10732	80	C	A	AGGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCCTTTAGTGGTCAGCCTTCCTTACCCCCAAGAATATCCCTGGTTTATTGCTGTGTCTTC ATTGGTTCACT[C/A]TTAAAGTTCTGTTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127	A	T	GGTTGTGTTTT CTGTATGTACA ACTC	TAGTCTTTCTTTGTACGAGTGTCATAAAGAATTACCACTCTGTCACATTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGCACACAAACATGAGGTTGTGTTTCTGTATGTACAACTC[A/T]CCAA CCATTAGGATTGTCACTCTCATATATAGACAGAATTCAGTGGTGGTGATTGAATTCCACACATGGA ATAAGTCTA
WI-11215	68	C	T	GAGTGACAATC CTAATGGTTGG ---	GAAAAAAAGTTTAATTGGATTGCTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/T]ATTTTTCTATAATATTTCTTGTAAGTGATGGATTTTCTATAAATTAAGGAAACAGATATT ACACAGAGAAGACAGGATTGCTTGAATTAGTAATACATTCTTTATTCCAAGCCCCATTCCACCATGT TTT
WI-11219b	89	G	A	GAGAGAATAT TCCAAAAAGT AGAGAA	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATTCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAGTGTAGAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGAGAAAAAATCCAC AAAACATCTC
WI-11219a	18	G	A	GGTCCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATTCCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAAATCCAC AAAACATCTC
WI-11222b	136	G	A	CATACCACTGC GGCTGG CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGGGCTTTGGATTTTGT TTTTGTTTTTTCCATAGACCCCACCGTTGAACTATTGTTAAACATTTACCAGCATACCACCACTGCGGCTG G[G/A]TCACAACTTGGCTACCAGGAGAAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGG AAAGCC

ID	No.	Allele		Flank 5'	Flank 3'	Sequence
WI-11222a	25	C	T	GCCACAGTGGAATCATTTACA	TTTTAGCATTGCTGATTTCG	AGCCACAGTGGAATCATTTACACTA[C/T]CGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTTTGTTTTTGTTTTTTTCCATAGACCCCACCGTTGAACTATTGTTAAACATTTACCAGCATACCACTGCGGCTGGGTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTCACAGGCTACTGGAAAGCC
WI-10775	39	C	T	TTTATGCCATATTAATTCATTACACTC	CTAGATGTATTTGCTAAGAAAATATGATG	TTGCAAGTTGTTTATGCCATATAATTCATTACACTC[C/T]TACATCATATTTCTTAGCAAATACATCTAGACACCTGGCACTCAGTAAGGGATATTCCTGGCACGAATAATCATTGTTATCATTAGACATTGCAGGAACCACCACCATATGGATGGTGATAAATGTGTTGTTTTAATGAAGGCAAGCAATTA
WI-11226	165	A	C	---	---	TTGCATGCATTTATACGAAAGGAATTAAAATATCTTCCTTATAGTTGAATTTTAAGTAAAAAATAAAGTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATTGTCAGTGGTTGCTAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCCACAAATTATTTCATGA
WI-10778	62	A	G	GCAAGGGAGGAACATTTACAG	CTGGTGACATCAGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAGGAACATTTACAG[A/G]GTCCATCTCTGATGTCACCAGCAGGGCCAGGAAGGGTTGATCTGGAG
WI-10789	21	C	T	GGGACACACTGCTCTAGACC	TTGAGGGACCCTGGGA	TGGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCTGCCCTGGGGACGCAGAGCCAGGGCATCAGGCCTTAGTCCTCCTGGGGACAGTGAAAGGGCCACCACC
WI-10810	58	C	T	CATCTTCATGGGCAGGAATT	CAAACCCTAAGAAACACAGAAATG	ACAGAAAAAATGCCTAGGTCTTGTAGCAAGAGGAAAGCATCTTCATGGGCAGGAATT[C/T]CATTTCTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCCCTGTCCCCTGATCCAGCAACATTTCCGTAACTACCCTCTAGAAGTCATGCAAAGAAAATGATGA
WI-10828	23	T	C	---	---	GGACCAAACAGAATTACTTGGCA[T/C]AGGGTTCTTAAAACTATTCTGCAGAACATTAGTAAAGTTTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGAACATGTGGATGAATATTCTTTAGTAGAGGACTTCTAAAAGGCTATATATTTGGATACATTACCATTATGAATCTCAAAAGGAGCATGTAGTAGGGCATATCTAA
WI-10832	91	G	C	CATTAATCTGCAGGCTCTCC	CCTAACTGCAGGTGACTTAGAAA	TATGCCTTCCCAACGAGCCACCATCCACGCTGCTCTTAGCACAAAAAATAGAATACATCATTCTGAATGGGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTATACCATATAAATCTGATTTCTGAGCAGGAGGGCAGATGAGAGAGGCGTCTCCGTGAAATACTAGTTCGG
WI-10834	96	C	T	AGAATTAACTGTTCAAAAGTGTGTTAAT	TGGCCCTATAAAATTGGTATTAAG	GATTTGAGTATTATCAAAATTGCCCAAAGACCATTAACAAGAGATTTAATAGTTAAAGCCAAAACTATAAAGAATTAACTGTTCAAAAGTGTGTTAAT[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTTCTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T	C	---	---	GGATGATGTTCGTGTGGTCCCTTTA[T/C]AAAGCCTCTTGCATCCCAAATGTGTAAATTATTTATTCTTGGTATTTCTCGCTTACCCATAGTAGTCACCTGTCAAGTGTTCCACCCT

Name	Pos			Sequence (5′ flank)	Sequence
WI-2296	81	A	G	TGTTACTTTGATTCTTTGCTCTGA	GCAAATCACAC AGCTAACTGG TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CAGTTAGCTGTGTGATTTGCAGAAGGTTACATTTGTTTGTTG
WI-2300	77	G	T	GGCACAGAAG GGTGGGTCAA TTTTAAAGCA	CCAGTCATAC TTTCATCATGCTGTCTTCCCTGGAAATTTCCTTATTTGAGCGGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCTTTAAAATTGACCCAACCATTACTAAGAATAGCATTCA
WI-2371	55	G	T	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC TCTCTCCGTGTCTGTGTG CAATGATCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTTCTTCCCAGCTTCT[G/T]GTGTGGCT GTCAATCTTGACATCCTTGCGAGCTGTATAATCCTTGCCAGCTTTACATGATGT
WI-2395	122	A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA GGGGGCACAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAATATCATAATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAA[A/C]CTGAATTC AGAATAAATAGAAAGGTAAATTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192	G	A	...	GTGCCAAGGACGCATTATG CACCAGCCACCACCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCGAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG
WI-2437b	179	G	A	...	GTGCCAAGGACGCATTATG CACCAGCCACCACCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAGACACCAAAAATTCCCAATGTCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGGCTGTG
WI-2437a	128	G	A	...	GTGCCAAGGACGCATTATG CACCAGCCACCACCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGGCTGTG
WI-2440	71	G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACTCTGC TATTGGTCTCA C CAGTAGGAAACGGGTTCTTCCTTAGACCCTCCAGAAAATAATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123	T	C	TGTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAACAT G CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATTGTCATACTATATTGTTAGGAAATAATGACAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAGCCATTTTCCCCCAATATTTCAATCCACCACAGTTGGTTTAATCCACAG
WI-2886	46	C	A	CAGAGTCTGG GGGGAGAAGA	TTGCCATGCTT TATCTCGTT ACAGTTAAGAAGAAAAGGCTGCAGCCGGTTGCAGAGTCTGGGGGGAGAAGA[C/A]AACGAGATAAAAGCATG GCAAAGACCACGCTGAAAGTATCCCAGGGTGCTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGGCTAGGCAAGGAAAGGTGTCAGAAGAAACAGAGAGGAGCGTT

ID	#					Sequence
WI-2906b	77	T	A		...	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGGAACTTGCCTGGGAATGCTC TTTCCCTC[T/A]AGAGCTTTGCTTGGCTTACTTTTCTTTTCCTTAGGTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-2906a	50	A	C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGGCTT[A/C]ACTTTGCCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCTTAGGTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-1736	175	C	T		...	TACTCCTCATTCCTCCTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCTAAAT TAGAATTCCCACCCCCAGCAACTATTTACACAGAAACAGCAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGCAGTGGTTTTCCATCTGTCTTCCA[C/T]AGAGATCTAGGGTGTCTTGGAACC ACCTTGG
WI-1851	136	G	A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGGAGG ACACAAACATTAGACCATAGCCATTGAATTAACTATAGATGTGTTAAGTAATTAATTAACATGGTA CA[G/A]ACAACTTCAGTTAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACACTCATG TGA
WI-3000	62	G	A	CCCAAAACAC AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGGAAGCACTGTCTTACATCTCTAAATGTCAGCACCCAAAAACACAGAGACCCC[G/A]T GAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G	A	TTTTCTCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCCGCCACCCCGGATTATTTACT TAAGGGTTAGCAAATTCACCTGACAAAGAGTTAGTTTCAACATTGACCCTCATAAAGTGATTTT TTCTCTTTCTGTTTGTTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATCGACTTTCTGT AGCCACAAGATT
WI-3167	37	T	A	AAATTCAACC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCAACCACAGATCTATTAGATTC[T/A]CACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G	A	GTGGGAGTGGGC AGATAAAGA	TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGGAAGGTGGCAACTTGCGCAGCAGAGAGGAGGAAG AAGTTCAGACCGTTGGGTAGGATAAGTAGTGGATCCAACCCCTTTGTAGGGCAGGTGGTGGGGCGCAG ATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGTGGGGATTCAAG
WI-1775	47	C	T	CCTGCATGGTC TTTCTCTG	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAACCCTGCATGGTCTTTTTCTCTG[C/T]TTTACATCATTGTCATA AATCTCAACTGACACATCAGTCTCTGCCACCCCA
WI-3402	55	G	A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAAA AAGGAGCATTT G	CTGCCCTTACATCCAAAGCCAGTACTCGAGCATATTCATTGATTTCCTTACAT[G/A]CAAATGCTC CTTTTTAAGTCCTCAACTTTAAAGCGGAAGCATGCACAAAATAGATTTCCTTAGGA

Name	Pos			Primer 1	Primer 2	Sequence
WI-3416	33	C	T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTCAGAAGTC[C/T]CTCTTAGAGGTAGTTGTGCTCGTCGTTAAAA TATGTTTCAAGATAGTATCTCCCTGTTGTCACTTCCTCCAAACAAGTGTACCAACACGATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGCACACATAATCCCATTGCCTAAAAAGACCAGG
WI-3453	70	C	T	TTCTTAGGCCC ATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTAACAAATTGAAAATCAGCTACTCTTCTTAGGCCCATCAGAG AAT[C/T]GAAGTCATGGGGAAAATTGATGCCATGTGAATTGGAGAAACAGCAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCGAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G	A	...	...	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTTAATGAGGTGGT[G/A]TGGGAGAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A	G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCAC[A/G]TGTATTTTAATGAGGTGGTGTGGGAGAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79	C	T	CCTGGGTTTCT GGGATGTCT	GGGTGACCCTG TCCTCA	TTTGACCCCATACATGAGAATAAAACCATAAAGAAATGGTGAAAAATAAACGGGGAGAGACCTGGG TTTCTGGGATGTCTC[C/T]TTGAGGACAGGGTCACCCAC
WI-3600b	146	G	C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCGCAGCAGTGTCCTTGACTCCTGCCGTTCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTCCTGCTTAAGTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3600a	78	T	G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCGCAGCAGTGTCCTTGCCGTTCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTGT[T/G]GAGCCACCTAAACTCGTTCCTGCTTAAGTATCCAGAGGTGGTTTCTAACCTGG ATATAAACATGATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3678	125	G	T	...		TAAATCATGCTATTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCCTGAACCTTCTACTTACTGTGCTGTTATGATGCCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTACCTTGTGTTGTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67	A	C	...		AAAGCGATGTTGAGATACCACATTCCATGAAAAGTAAAAACACACAAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCCAGAATACTCCTGTCATTCTTAACTTTGACTGCACAG
WI-3735	72	T	C	CCTCAGTTATG TATCAAATGA AAAAC	GGCTCACCAAT CATTGTTTT	TCTAAATGTGAAACCAAAGAATCCTGACGACCTAACTGCCAGTCCTCAGTTATGTATCAAATGA AAAAC[T/C]ACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC

ID	Left	Pos	A1	A2	Right	Sequence
WI-1819		51	C	T	...	GAAAAAGCAGGAAGCCAGGCAGGACAAACTTTGAAAAAGTCTTTCAGCAC[C/T]TTCGTGGATCCG AATTTTAGTGTGTGATTGGCAGGCAATGCGGGGTAACATGTTCCAGTGTTTAACTCTGCACAGAATTGC CAGATTAGCGATTGTTTGACTGTTGTCCAATTAATGAAATGTGGAAAAAAAAGGGGGTTGGTAACTGTT AAGCCTGCTGCAATGTTAGACACGAGCTGGGTGGGGAGGTGGAATACC
WI-3746		116	G	A	...	GGCCTATTCACATGACACTGGGCCAAGATCTTGCTTCCCTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCCAGGAAGAGATGGTTGTCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	ACAGTCATTT AGTCTTCCTGA CAA	49	T	C	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCTTCTGCTATAG CATC
WI-3898	TGACCAATGTC TTTAGAAGCA G	25	A	C	TCGTCGGTGTC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGGAGAGGAGGACACCGACGAGAGCACACAGGAAGGAGTGAG GTGAAGATGAAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
WI-3901		114	A	G	...	GGACCATTGTCCCTCAGAAGTACATTCAAGCCCTGGACGGTGCTGCCTACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCTGAACCTGGCTTCCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	TGATTCTTCTC AAGACTCACA GC	99	C	T	TCTAGAAGCAA TGAAGGATGG	CTGAGGGAGATTGATGCTACTTTACCTGAGGAAACTTTATTACCTCCCCTGAGTTGTTGTTGCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	CCAAGAGCGT CCTATGAATC A	33	G	A	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTTGTTCCTGTTATTGCTGTTCACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	TTGAGGTCTTA GTCATTGCATG A	84	A	T	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTTGTTGTGCATTTATTGCTTCTCTTATGTAAACACAATCACCAACATTGAGG TCTTAGTCATTGCATG[A/T]TGTATAACAATATTGCACTTAATAGGAACTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	CCTATAATTTA GCAACAATAT CAACAGAA	117	A	G	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCTTTGAGGTTAGGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTTGTTTCCTATAATTTTAGCAACAATATCAACAGAA[A/G]GGGCTATATTAGAAA ATTCTACCTGCATCCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	GGTGAGAGTC AAATTGATAC AAACA	32	A	G	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGGAGAGTCAAATTGATACAAAACA[A/G]TCTGAAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTCACTGCTGGGCAATTACCTAACATAAATGAT

ID	Pos					Sequence
WI-4177	68	T	C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATATACTTTCCAAATGACTAGTAGTGATGAATAAGCACGTATTAAATTTACCTATTATATTT AT[T/C]CATCATGATTTGCTGCCTTCTTCTTCCAAATTTACTACAAATTGTATTGTCACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51	A	C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACTCCCCAAGTTAGTCAATATAAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACACAAACAA
WI-5163	24	C	T	CTGTCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCTGT[C/T]GGTCTGTTCCTGTGTCCTTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117	A	G	---	---	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G	T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G	C	TGCTCCCCCAT CACCT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGTCCTGGGGAGATAATAGGAAAGGTCCCATCCCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CCTTACACAACTTGAAGTAGGCCCCATCCAAACACTGGTCAGAAGAGTAATACTGTCGAC
WI-4256	57	C	T	---	---	ACAGCCTCTTCAAAATGGCACAATCAAAAGCACCAGTAAAAGCAGGAGGTAAACATCTGG[C/T]CTCAC CATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAATGATTGGCCTT
WI-4325b	71	C	T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTCTTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA GATG[C/T]TACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C	T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTCTTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A	G	---	---	TGGGCAGAAGTGCGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTCACCTTCT CTAGACTCTTGACCCTGTTCAGGAGGATCCCTGCCTCTGAGTTTTATCATCTCCCACCTCCAGCCCAG GGCCCTGTATCGTTGTTCAGGCCCC[A/G]GAATCGTCACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117	T	C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCCTGGTCGTGTTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACGACACAAACCAGTGGGACACCAGGGTACTTGTATCACC[T/C]CTCCCGCAACCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGAGAGA AAAGAGGGACTTTGACACACAACTTGGA

Clone	Pos	A1	A2	5′ flank	Sequence
WI-5204	54	C	T	---	TAGATTTTGATTGATGACAATAGGGAAGCCTTGTTTAAATTGGGTTTGAAGAA[C/T]GAAGAAAAATGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTTGAGGGGCAGCAAATCCCAGTTTGACTGGAATATAGAGTGTGATGTCAGGGTTG
WI-5215	70	A	G	GGACCTTAATATTTAACAGACTCAAAA	TTTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAATAT[A/G]GCGAAAACTATCTTACAAAATATCTCCATAGCAGTAGACATTTTAGCACATTTCCTGTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T	G	TTGTATCAAAGAGATGGGGTATATAA	CCCTGAAATGTGCTTTGCTTCTCCTCCAACTCTCTAGGGAACTTTTCCATGTCAGGTGAAGGTTTTGAAGAGTACTTTAATTAACTTGTATCAAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTTCTTTAATTAGTGAATTTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49	C	T	AGTTGAATTATTCAGAAAATTTATAGTTCC	ACACATTTCATTTGCTTAAGTTGAATTATTCAGAAAATTATAGTTCC[C/T]CAAGTTCATGCATAACAGGAAACACCAGGTTGGGGCAATTGATTGAATTGT
WI-4461	49	A	G	TCACTGTTATTTAAAATTATCCTTCC	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTAAAATTATCCTTCC[A/G]TGAAATTGGTGAAGGTCAAAGAATGAAATTCCCCACTTTATTTGGAAATTTTATTTGGGATGATAATGCAATGGGC
WI-4465b	75	G	A	---	CTACTGGATTTACTTTGCTCAAGCCAGACAACACGAAAGTATATAAAGAAACAGTTAGTAATCTTTCACCTTT[G/A]TATTTCTCTCTCTACCTCAGGGAATC
WI-4465a	41	A	G	AAGCCAGACAACACGAAAGT / GGTGAAAGATTACTAACTGTTTTCTTT	CTACTGGATTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAACAGTTAGTAATCTTTCACCTTTGTATTTCTCTCTTTCTCTTCTCTTACCTCAGGGAATC
WI-1949b	160	T	G	GAGTGAATAAATGAATGCCATAATC / TGAGAGGTGGGGACAAAAA	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCATGGCTGAATAAATGAATGCCATAATC[T/C]CTGTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGGCACA
WI-1949a	86	T	G	CAGTGGTGGAGATGCTCTGAGTGCCTTG	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGGAGATGCTCTGAGT[T/G]CAAGGCTGCTGACATGGTCATGGCTGAATAAATGAATGCCATATATCTCTGTTTTTGTCCCCACCTCTCACACCTTTCCCTGGCACA
WI-4529	64	T	C	CCAAGTAAGTCTATCATTCTGAACACTCCTGAAGATG	TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTCTGAAGATG[T/C]GAGTTCTCTTTTTATATCCTATGATTATTTTAGAATATAAACTCCTGGGTCGCTGGACAAGATGGGCCCTAGGATCATTTT

Clone	Pos	Allele		Flank 1	Flank 2	Sequence
WI-4540	110	A	G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCAGTGTCCAGTC AAATGAGACAACTTCCTAT
WI-4582	226	T	C	---	---	AGCAAGGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGGGAGACAGCATTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AATAACTTTATGGGAGAACGCTTGCAAAATATGGTT[T/C]CICCTTGCTAGAAACCATTGAT
WI-1965	105	G	C	GCCATTGAGG AAGTGTTTAA AG	GAATGGGATGGG TCATCTCTCT AG	CAAAGGTTAGTTAACTTGGGGGGCAAACACAAAGTTATGAGTAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTGTTTAAAG[G/C]AGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATCTATTCCACACAGATGTGGAGTCATTTATTTGGTGTATGACAGT CATGG
WI-5248b	99	C	T	CACTGTTTTCT ATTGACCGTAC TTG	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCCAGAAAATTAAAACGCCTAC CATTTTTCACTGTTTTCTATTGACCGTACTTG[C/T]TCTTGCTTTTTCCCTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G	C	AGTTTGTGCTG CTACGTTGTT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTA[G/C]AGCAACCCCAGAAAATTAAAACGCC TACCATTTTTCACTGTTTTTCTATTGACCGTACTTGCTTTTTCCCTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T	A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGCTCTGAAGCAGAAAGCACTGTGA C[T/A]CATTATTAGGCCCATCTCCTGCCTGAGCCTGCCTCACAGCAATTGTAACATATGGCATTGGG ACATATCTCTGAGCCGATCAACTATTTGACAAGATTCTCCTTTTTAACAA
WI-5252	119	A	C	---	---	GAAAATAGGGCAAAATTAAGGACTTCAATAATTAAGAAGAGTCTTGGGAAAAGGATTGTGATGATCATTG AATCTGTTTAAAATACAGAATTAATACTGAATACCTGTGTAAATCATTGCTTT[A/C]TACCCATGTACA TATTATATGAATTAACAATGTAAAATAGTATGACTAAGAAAATATTGGGCCCT
WI-4606	61	A	G	GCAATGCTAG AAAATTATGC CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA[A/G]C CAAGTAGCAACTTAAGCACCTAAGGCAGAATGAAAGTTTCTCTGTCATTAAGTCCTCTATTCA ATTACCATTTATCGGGGTAATTAAACACTGGAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCTTTGCTATGCT
WI-5257	77	C	A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGCAAATTAAGCATATGAAAATACCAAGTGTTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTTCATCTGCCCCTGGTGGTTTTTCAGTAGTGCAACTGCTTTTGCCTCC CGGATGAAAAGATACCCTTCTATGACTCAGCAATTCCACTCCTAGGTATGCACCCTAAACATGGGTG GCAAAT
WI-4649	50	C	T	GAGACCATTCT TTCCGAATG	TGTACTAGGTG TACTTACAGA AATCATC	TCACTGTTTAGAAAATTTCTTCTTCCTCAGTGAGACCATTCTTCCGAATG[C/T]GATGATTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAGTACTTGCTACCTGAATTTGTATTTTTTTAA AAAATCCTCCCAATATTG

ID	Pos					Sequence
WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCTT	CTGAAGTGTTA AACTGGATTTG G	AACTGTGTGGTATGTATGTTGTTTGTGTATTTTCTGGAGAGTCAGTTACTCTCCACTAGATCATAAAGGG GACTTGGGAACCAAAGAAGCACAAAGAAGTATAAGTTGTCTC TTATATTGCTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTGAACATACGTCGACATTTGGAAAAAATTGTCCAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACAGCAGGTTTATAGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATTCTGTAGAAATTTCACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTCTTTGACGGAAGAAAACTTCAA[C/G]TTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC	AATATGGAATC TGCATTCAGTT G	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAGATGGGAGATTATTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTCAGAAAACGTGAAATTATTGAGTAACCATGGG TCAACTATGAT[C/A]CAAAACACAGCAGTGTTGTTGTCTAAAAAATATGATAGTTTCTTCTCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTTACGTTC CCTGTCTCATC GAA	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGGCACAGACAGGCATTGTGTGGCCTGCACAGGTGTTGTTGGTTTGTTGTTTGTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAAGTGGCTCTCAGTTACTACAGACCTCATCATCCTCGGTTCCTTG CACCCAGTCCACTTCACGTTCCTGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTCCAAGGTTATACAGGACCAGTGTTGGAACC AGCCATTTCTGGGGTTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGGAAGGACAAGAGTTGAAGCAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCACCAGCCTCCTTCCCACCATTCTCCACCTTCTACTCTGA[T/C] AGGCAGAACTTATATGGAAAAAAGGGA
WI-2034	150	T/C		CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACACCATGTGGCGCCAAGA CCTCCTTCTCTGCGGTTTCAGTGAAAAAGACGATGAACTCCTTCATCTTCTACAGCAGCTGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACTCTATCTTTACCCCTTCCGACACCACCCAGATGCTGAGATGCC ACACTCTGAGTG

Marker	Pos	A1	A2			Sequence
WI-2038	155	C	T	TGTGCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAGAAAAAGTCACATTCTTCAATCACTCCACCATTGTCTGTTATTGTCTCTTGCAGTGT ATCCAAGGATGTCACTTTTGGAACTCTGTAGATCAGAAAACTGTCTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTGATA[C/T]TGATGTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTCCATT TGCATTCCATTGGC
WI-4782	113	C	T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATTCTTAGGAAAAACTAGGCTAGGAGAA CACAATTCAGGTCTCTCCAGATGCAGAAGATAACTAGAACAATGC[C/T]GAACAGAAAATAACCA GAAGAGTCATTATGGTTTTTTCCAGAACGATTAC
WI-4788	65	A	G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAATCATCTTGCTAAGTTCC[A/G] TGAAAAAAATTATGCCAAATTTAATTTATCCAAACTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T	C	TCCCAGAGAC CACTTCCATTC	CTACTCTTCT ATTTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCCAGAGACCACCACTTCATTC[T/C]TTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G	T	TGATAATGGG GCCCTGTT	CCTTCCTTTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATTCAAGAGGAAAATATACATATGGGGTGATAATGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A	G	TTGCCATAGAC TAGGTTATGTC C	CATATGTATAT TTCCTTCTG AATAAATT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATTTATTCAAGAGGAAAATATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T	C	TTCCATTTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTTCCATTTGTTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTAAATTAATAGCAAGGTTAAT AATATAATAATGATGTTATATATTACAATTCAACTCAACAGGAATTCCATTTCTGGTAGCAGGT ATA[T/C]TGGACTCATTTCTTCTTGCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G	A	GCAAGATATA AAGATTAAGA AAAGATAACA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCAAGTTACTCGGCAAGATATAAAGATTAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAATTGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A	G	---	---	AACATTTTTAACCATGCTACACTTTACAAACACTGAAAAGACAG[A/G]AAAAAAAGAATATTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAAAATATGAATCAGAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	A	G	---	---	GCCTTTTTGAGTTAAGTCTTTTTGAGTGTGTCTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAAT CCCCAAAAGAAAATAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	G	A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATCACTCAGCTTTGCTATATCACTCCACT GAGGTATATTCTGTCTGCATTTCTATATCACTCAGCTTTGCTATATCACTCCATCCACTCAACTTGCAG

Name						
WI-5370	143	T	C	CAAAGTTGGTA CAGAGAATTTC AAA	AATAAGATGG TACCTTAACTA ATAAAACAA	TGCATGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAAAATTACCTGTATCCATCATGGTTCATTGCAAAAAATAAGATGGTACCTTAACTA ATAAAACAA[T/C]TTTGAAATTCTCTGTACCAACTTTGCTTTTC
WI-9711b	423	T	A	---	---	GATCTCCTTCATCCCTCTCCAGAGAGAGGAGAAGAGAAACACAAGAGAGAAACGCCTGGTGGGGAAAGCAC CCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGAGCGGCTTGCTGTATCCTTGAAGCGTGTGCAGCAGCTT TGGACCTCAACAGTTGTAGTTGTAGCTGTCTCGTATCCTGATACTCTTAAAATTTGAATG CAGTTTCTTCGCCTGTGGAAAATATTTTCCCTGATACTCTTAAAATTTGCAG
WI-9711a	390	C	A	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTGTATTCAGCAATTCCTACTCCTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTCATTCCAGTGCTACAGCATCTGATAG CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9702c	345	G	A	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTGTATTCAGCAATTCCTACTCCTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTCATTCCAGTGCTACAGCATCTGATAG
WI-9702b	344	C	T	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTGTGCCTATTCAGCAATTCCTACTCCTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATT[C/T]TAACTTTAATGATCTCTGTGA CTTTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG
WI-9702a	179	C	T	---	---	TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGGGTGTGATTTGGT[C/A]AGCATATCTTAGGT ATATAATAACTTTGAAGCCATAACTTTAACTGGAGTGGTTGATTCTTTTTAATTTTATTGGGA GGGTTTGGATTTAACTTTTTTAATGTTGTTAAATATTAAGTTTTTGTAAAGGAAAACCATCTCTG TGATTACCTCTCAATCTATTTGT
TIGR-A003N21	49	C	A	---	---	AGAATGGCTACTTCATAGGGCAGAGCAGCAGCCACTTTGGCTAATTTTTAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAATAAATTATGTTCTATTTGGAATACCTAACTAATATCAG ATACTAACAAGTACACAGTGATAAGAATAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGTA AAAG[C/G,T]CTTCTAGGTTAGTTAGTAGAAAGTT
TIGR-A004V30	203	C	T	---	---	G

Name	Pos				Flanking seq	Sequence
TIGR-A004W22	232	C	A	---		GGATAAATCAGTACAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGGTGGGAGGGGGCTGGGCAGTG CCCGAGGCAGGGAGGGAGGACAGGTGGGACAAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTTCCCACATCACGACCCCGCCTA[C/A]CTGGAGATGTCTCTAAAA GCCTGCCCACATTGGTGCTGCCCCCGCCTA[C/A]CTGGAGATAATTCATTTGATTTCATATTC
TIGR-A005D24b	138	C	T	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAAACCCAATTT CTTC/T]TTTCACCATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
TIGR-A005D24a	123	A	G	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT[A/G]AAAACCAA TTTCTCTTTCACCATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
U03735	74	C	G	---		TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGGTCTGGGCCAGTGCACCTTCCGGGGCC GCATCC[C/G]TTAGTTCCACTGCCTCCTGTGACGTGAGGCCCATTCTTCACTCTTGAAGCGAGCAG TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTGTTGGGATGACTTTGAGATTATTCTTGTTCCTGTTGGA GTTGTTCAAATGTTCCTTTAA
U39840b	42	T	C	---		GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT[T/C]CAACAGCAAACAAAACCACA CAAACCAAACCGTCAACAGCATATAATAAAATCCAACAACTATTTTATTTCATTTTCATGCACAACC TTGCCCCCAGTGCAAAGACTGTTACTTTATTATTGTATTCATTGTGTATATTACTACTACAAA GACGGGCCCCAAACCAATTTTTCC
U39840	56	A	C	---		GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCCAACAGCATAATAAAATCCAACAACC CAAACCAAACCGTCAACAGCATGCAAAGACTGTTACTTTATTATTGTATTCATTGTGTATATTACTACAAA TTGCCCCCAGTGCAAAGACTGTTACTTTATTATTGTATTCATTGTGTATATTACTACAAA GACGGGCCCCAAACCAATTTTTCC
WI-8997	41	G	A	CCCC	GCCCACTTGCT TGTTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCCCTGCCCACTTGCTCCCC[G/A]TGAGCACTGCGTACAAACATCCA AAGTTCAACAACCAGAACTGTGTCTCATGGT
WI-7008	180	A	G	---		TATACCACTTCCATTTGATGATGGAATGCTGCTGTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTCAGTTCATGATGATAGGCAGTTCAGGTCAAACATTCAG TTTCCACCAAAGCCAGTAACAGGGCCAAGAGCTGTCTCAAAAG[A/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGCCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C	T	TCCCAAAAGTC TTAAGAAGAA AAA	GGGAATCT CGAATTTGCTG	GGTCCCACGAATTTGCTGGGGAATCT[C/T]GTTTTCTTCTTAAGACTTTTGGGGACATGGTTTGACTCC CGAACATCACCGACGGCGTCTCCTGTTTTCTGGGGTGG

ID	Pos	Allele 1	Allele 2	Flanking sequence 1	Flanking sequence 2
WI-7593	46	G	A	...	TTTTTGTTGCTCTGGACACCCACTGCTCCCAGGATGAAAGGAGGAG[G/A]AATGAGAGATCAGTTTTGGACACTTCCTCTTGAAATATAAAAGAATCAACAAGTTACAGTCATGTTGGGGACTTCTCTCTCCAA
WI-6962	78	A	G	...	AGTGCATCTTGGGGGGAAAGGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTCAGGTGGGACTCTTGATCCAGAGA[A/G]GACAAAGCTCCTCCTCTCATCCTATCATCATAGATAACATTCTCCACAGCCTCACTTCATTCCACTGACTCCTGGCCTTCTATGCCCTCTATCATCATAGATAACAGAGAGATTTAGATAAGACTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-7059	43	C	G	AAGGCACCCA GCCATC	GCAGAAGAAGAGAACCATGCCAGGGGAGAAGGCACCCAGCCATC[C/G]TGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCAGAGAAATAAGAAATAAA
WI-9063	53	A	C	CACTTCACTGA AAGACACCAT TT	CTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCAGAGAAATAAGAAATAAAGATGAATTGTTGCAACTCTTAAAAAAA AGCAGCCATCACATGATCTGTTTTCACCACTTCACTGAAAGACACCATTATT[A/C]TACCCAAGGGCAGAAAGTAGAACTTACTATTCATTAAATGTTTGACACAATTGGAATTGTC
WI-7079	293	T	G	...	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTCTGTAGAGTTGGAACTGCATTCTTTAAAGTTTTATATGCATATATTTTAGGGCTGCTAGACTTACTTTCCTATTTCTTTTCCATTGCTTATTCTTGAGCACAAAATGATAATTCAATTATTACACATTCAATTATCACCTTTTTGACTTTTCCAAGCCCTTTTTACAGCTCTTGGCATTTCCTCCGCCTGTGTGAGGTAACTGGGAT
WI-9074	38	A	G	GGTAAAAGTT CTTTTTGCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTTGCTCTAAAAGAA[A/G]AAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTTAAGGATGTTGCCACTGCCAAATGTAACTGT
WI-7104b	249	C	T	...	GGAGTTTGCCCCTTCCTAAGGGAAGGAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTTCACGTTGGGAGAAGAGAGTGCCAGGAGACCCTGAGGGCCAGCCGGTTCCTACTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCAGCATGAGGGCCCAGCCAAGAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGGCCTTGCACCAGGTGGGGGCCCACCAGCCATCTTTG[C/T]T
WI-7104	157	C	A	CCTGAGCCCTC TGTAGGGCTGA AAGAACTCA GCTGGC	GGAGTTTGCCCCTTCCTAAGGGAAGGAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTTCACGTTGGGAGAAGAGAGTGCCAGGAGACCCTGAGGGCCAGCCGGTTCCTACTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCAGCATGAGGGC[C/A]GCAGCAAGAGGGCTTGGGTTCTGAGGAAGCAGATGTTCATGCTGTGAGGGCCTTGCACCAGGTGGGGGCCCTACACCAGTTTCCACCTGGAGTTCATGCAAGGGCAAAGGCAGTGCCATGCAAGCTGTTAA
WI-8974	34	C	T	CCTAAGCATTG GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTCCTGTCTCTGTAAGCCAAAGAAATGAACATTCCA
WI-9161	61	C	T	CCTAAGCATTG CCTGGC	CCTGTTCCCATCCATCTGTCTGTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGGCTGGAT
WI-9014c	93	T	C	...	GTCTCCATCTCTGTCTCAACTTA[T/C]GTGCACTGAGCTGCAACTTCT

Marker	Pos	A1	A2	5′ flank	Sequence	3′ flank
WI-9014b	44	C	T	...	CCCTGTTCCCATGCTGACCTGTGTTCCTCCCCAGTCATCTTTC[C/T]TGTTCCAGAGAGAGGTGGGGCTG GATGTCTCCAATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT	...
WI-7023b	206	C	A	...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTGCAGATGGTTTGTGACAGACCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCCTGTGTCTGACTTTGAGTGGGATCAACATCTGTCTCCCTTCCCATTCAACAC A[C/A]ACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA	...
WI-7023a	56	A	C	...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGTGACAG[A/C]CCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCCTTCACGGGTC CCTCTTTTTTGGGCCCCAGTATTCATGCCACCAAAGCTCTGGCTGGCAGCACTAA	...
WI-7093	54	C	T	...	CTGAAATCCCCTCTCTGCCCTGGATCCGGGGACCCCTTTCCCTTC[C/T]GGCTCCCAGCC CTACAGACTTGCTGTGTGACCTCAGCCAGTGTGCCGACCTCTCAGTTTTCCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAAAGCTGGAGGAAGGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTTGCCGCGGCTGTGTTGTGTTA	...
WI-9171	62	G	A	CTAGGACCCC ATTCTCCTATT	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAGAAAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATTCTCCTATTTA[T/C]CAGTCCTGTCCTATATA CCCTCTAGAAACAGAAGCAATTTTAGGCAGCTATGGTCAAATTGAG	TCTAGAGGGTA TATAGGACAGG ACTG
WI-9174	47	T	C	CCATGTTCCGA GAAGAACAGA A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGAT[A/G]ATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTAATGTTGGGTAGAA	CAGAGGTCTTG AAATACAGGG A
WI-7753	52	A	G	CCACTTCTCCC CGCA	AAAGAACTACAGAGGACGATGTCCAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTCAGACTTTCCCTTTCATCTT	AAAGGGAAAG TCTGACCTAGG T
WI-9186	76	G	A	AGAATATTGT CTGCCTTAAAG CGCA	TTGGACAAACCTAGAATTTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAATAA CTCAG[A/A]ATATTGTCTGCCTAAAG[C/T]GCTTTGGTTAATACAT	GGTGTGTGTGG TAGGGGG
WI-9193	94	G	A	CA	TTTTGGATTGATATCGTGAAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCCACCAACTAAGAA CTTTCCCTAAAGAAGAATAAACACAGGGTCTGAGGACGCCAC[A/G]GTCCCTAATGACACCCACTCCTAGCC	
WI-9015	48	C	T	...	GGAGCCAGGAGACAGCAGGGTCTGGGACTGGGGAAGAGTCCAAGGAGGGGAAGGAGGAGCAGCCACTCCTCAATGC	
WI-7254	37	A	G	GGTCTCTGAGAG AGGAGCCAC	CTGAGGCTTCGTGCCCCCTGAAATCAAGAGG TCAATGGCTGGCTCCCCCTGAAATCAAGAGG	GGAGTGGGGTGT CATTAGGGA

ID	Pos	Var	Sequence
WI-9231	32	G/C	CAGGTCCCCCA GATTGA — CACTTGCCCAC ACTCAGAC — GTGACCCTGTGAGGTCAGGTCCCCCAGATTGA[G/C]GTCTGAGTGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAAGATGAGGCTGAGAGCAGGGAGTTGAGGCCGAAGAAGTCA
WI-7836	120	T/C	CAAATAAACA ATGCAACGTTC C — GCTCTCAGAAC CAAGATTAGA AATC — TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTCATGGTGTCTATAACGTTCC[T/C]GATTTCTAAT CTTGGTTCTGAGAGCCATTTGGTTCAGTTGTAGCAATCCCCATACCAGCT
WI-7286	65	T/C	CAGCTTCAGCT TAACTGACAG A — AAACAATCTA ACCAGAAAGCT TTAA — TCCATTCCTTTGGCCCTGCAGCATGTCATGCTCCCAGAATTCAGCTTCAGCTTAACTGACAGAT/C [GTTAAAGCTTTCTGGTTAGATTGTTTCACTGGTGATCATGTCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91	T/G	CTAAGCATGT ACGTGAATTTT TAAAT — CCCAATTTTTA TTAAAAGTTTA CATCTAT — CAAATTCTTGGAAATATCTCAAATGTTAATAACAATGTTAAATTTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT[T/G]TATAGATGTAAACTTTAATAAAAATTGGGGTGTGG
WI-7860	50	C/G	A — ... — GAAGATTAAAGGGAGGAGGGTGTCTCTGTGGTCTCCTCCCCTCCCCCACA[C/A]G[TGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCCTGGACCAGCTACTGGGGCCTTATGGGGTGGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGGAGGGAGGAAATGGGTAACTCTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTTCTCTCAGGAGGAAACAGGGAGACCTGGGGTCCTGTGGAT
WI-9064	29	A/G	CGTACCTCCAA ACATAATTGA TTC — GCTTGAGTGTA AGTCTCGCAGA — CAAGGCCGTACCTCCAAACATAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCCTGGCTACTGTCTCTGCTCTGCTCTGCTTTTG CACACTTGTCTGTTCTTCAGTCCTGCTGGCAGGGTCCTGGCAGGTAAGCGCGGGGGTTCCACA GGGCCCCAGCCCTGGCAGGGGTCTGGCCCCCCAGGGTAGGCGGAGCAGTCCCTCCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAAATGTGACACACCCATCCTGAAGCGCAGCTTGCACCTCCAGT TTGCACAGGGATTTGTCCTGGGGGCTGAGGGCCCTGTCCCCACCCCCGCCC
WI-7307	128	G/T	... — GAAATGTGAC TTCACTTGGT — CAGGTAGAATT TTCTGTGTCCATT G — GAGGAAATGTGACTTCACTTGGTG[C/T]CAATGGACAGAAAATTCTACCTGTGCTACATAGGAGAA GTTTGGAATGCACTTAATAGCTGGTTTTACACCTGATTTCGGAGGTGGAAA
WI-9274	25	C/T	... — G — AATTCCTTTCTGGTAATCAGGCACATGAACTTTGATTAGTTGCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATTATCATAGGTGGACTAAATTCCTTATCATCTTATT AATTCAGCCAGTGTATCCACCAGTTTTTATGTTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTGTTAAACTGAATAGAATTGTATAGCGATGA
WI-7313e	266	T/C	... — AATTCCTTTCTGGTAATCAGGCACATGAACTTTGATTAGTTGCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATTATCATAGGTGGACTAAATTCCTTATCATCTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTGTTAAACTGAATAGAATTGTATAGCGATGA
WI-7313c	256	C/T	...

Clone	Pos	A1	A2	Flank	Sequence
WI-9281	68	G	A	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCCAGAGAGGCCTTGCTGGCTACTGG[G/A]TGTTAGTTTGCAGTCCTGTGTGCTTCCCTCTCTTAAAACTTGTAATTTTTAATTTACAAAAATATAA
WI-7848	142	A	G	GCTAACACTT TTAAAACCGT CTC / CATTATTTG AAAGCTATTCA GACA	TTCTGAAAATATAACCAGCCATTGAGCTATTTAAAAACTTGTAATTTTTAATTAATGCTAACACTTTTTAAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAACATTAATGCTAACACTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTCAAAATAAATGTGAAATGGT
WI-9304	70	G	A	GTATATTACA ATGATCACCG ACTGA / CCCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATTGCTTTGTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTTACAATAGTTCTGTGTGGGGCTGTTTTTTGT
WI-7933b	314	C	A	---	TTACAGAAACTTGCCCTGCTGCCTGTGTCCCCATGCTAGGGGCGGAGGGGTCTTTTCCTTCCTTCTTCTTTCC TACCTACCCCTTTCTCTTCTTCTTGGCCAGGGGCCTCGTATCCTACCTTTCCTGTCCCCTGGGCTGCTGCGTGCAC AGAGGATTGCCCCCTTCTCTTTTCAGAGCTGGCCCTGGATGCCAAATTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G	C	---	TTACAGAAACTTGCCCTGCTGCCTGTGTCCCCATGCTAGGGGCGGAGGGGTCTTTTCCTTCCTTCTTTCC TACCTACCCCTTTCTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTTCCTGTCCCCTGGGCTG CACAGAGGATTGCCCCCTTCTCTTTTCAGAGCTGGCCCTGGATGCCAAATTAGCATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTGGGGAGGAACCATAGCT
WI-7374	182	T	A	AAATGAAACTT ACGTTTTGTTG TG / ---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAAGAAGTACTGTATATTA AAAGTTGGTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTGT[T/A]CAGAAACACAAGGCTT GAT
WI-9343	78	C	T	CCAACAACAT CCTCTGCCA	GGTCTGCTCCTGCTACCTTGACCCTTCCCCTTCCTCTGCTTCTCTCCTCATCATCCCAACAACAT CCTCTGCCA[C/T]ACAACAAAACGTAAGTTCATTTGGGCAAA
WI-7386b	104	T	A	---	CTATATGTGAGAGGCGTGATATCTGGCGTGGCTGGAGGTTGGCGTGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A	G	---	AAGAAGGAGCTCAGTTACGGGGGTTTTTAAAACCTTCATGAAAACCTGAAGAGTTCACTTTTGTTATTAT GCTCCTTA[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T	C	CTTTAGAAAA TCTGCTTTAAC TTGG / CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTCTGATGCTTACTACACATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGG[T/C]ATTCCTCTAATTGTTCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T	C	TGCTGGGCTGT GTTCC / GGTCCAGAAGA GCCCG	TGCTCCCTGTCCCATCTGCAGTGACAGGGACCCCAGGCACCCCCCTTTGAGGAGGTGGGGTGAACTGCTCCTT GGCAGGGATTTGTGACACTGCATTGCTGGGGCTGTCCTCGCTTCTGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGGTCCTGTATTTGGGGTCTGGGAAATAAGGCATACTGTCT

ID	Pos	A1	A2			Sequence
WI-7424	131	T	A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGGGGGAAGAGCAGAAGGTTAGAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTCATTCGTCATTCCAAGAGAGAGAGAGAGAAAGAAAA [T/A]ACAACTTTCATTCTTCTTGCACGTTCATAAACATTCTACATA TCCTGCAAGAAGTTCTCAAGCCTTTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTTCTTCTCTAATTTAAGTGAGA[A/C]TCTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAAATTATGTACCACTCGTTTATTTGTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
X86400	118	A	C	---	---	GTGGCCACTACATGTTATAGAAACCATCATCATCTGTCACAGACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAGCATTAAAAAGTGTCCCATTAAAAGGACTTTAATCAACCTAA TAAACTCTAATTCTGCGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAAGGGTCACA ATTAATTCTTTGATCTTTTTACTCACTGTTAACTTATATAA[T/A]TTCAGAAC
WI-8053	242	T	A	---	---	TACACAATGAATTGCTTTTATTCGGTATGCATCCACATTCAGCATTTAGTGGTCCTGAACAGCAAG TGGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCCACCACATTCGGGGATCGTGCTGTGCACCGG GTTCCTTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCCACCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTTCCAGTGTCAGTGTCAAACTAGACCCCA
WI-6190	165	G	A	---	---	AACAGTCACCACCAACCACATGACAACTCGCCAGGCAGGCCTTGCTTCCCTCCCTCCTTTGCGTCCC ATGTGTCCTAGTCAGCAAGGTCGGGGAGGCACCGATGTTAGCTTCGCCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAAACCTGGACAGGCTTTCAGCACTGGACAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGTCTGAA
WI-6275	148	G	C	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTGATTGT[G/T]GGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCACAAAA GAATATTTGGGGCAGAACCCTGAACTGGCCACCAGGGACATCCCAAATATCCCCTCCCTCCTCCAGGG CTCACCCCGACATCCCTCAGCCAAATGAAGGCTCTGAA
WI-6421	41	G	T	---	---	GGGTGAGACGGGGTTTATTGTGCACATTTACACAGCGTCTGGGCGTCGCAGCGCCATGCTC CTGTGGTCGGCGTCGGGCGTTCACTTTCTTCACCACACATTTTACTATCAGTGCTCCAA GGTGATGGGCTACAGTGTCGCATCAGTGAGTCGTGTACACACATTTTACATAAATTACACGACTC ATACATGAAAA[T/A]AGAGCCTAAGGGCCTGTATTTAATGAGAAAAAA
WI-6905	215	T	A	---	---	AACTTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTGTAAAGTCAATGACTGTGTTGTTTT TAAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAAGGATACTGCAAGGTGCAAGGAAACCGAACCCATTGTTGTACACTGTTCTTCACACAG [G/A]GCATTCTTCTCACCTTAACTGACGTGTGCAAGATGCCTCAGTGTG
WI-9420	202	G	A	---	---	

ID	Pos				Sequence
WI-9448	184	G	A	---	TGGGGCTGCTTTAGAACTTCATTTCTAGAGACAGAGCACCTAGTGAGAGCAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTGGTTCCAAGGCTGGAGAGCTGGCCACCAC[G/A]CACTGGTTTCTAAA TCTCTGCTTGGATTTTATCCAAGCGCATGTTCCTAACGTGCCCGTGAGCAG
WI-9470	204	G	A	---	ATGTCAGAAGAGACAGACAAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCAACTCATCTCCTCAAGCTCCCAGGGCTCACCTTCCCAAG
WI-1245b	201	G	T	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTCAAGCCTCATAAGGAAGGAGTAGGTGTTAATGGCA TCCTAGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGTGGT TTATTAATTTCATTTCATTTATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC T]CTAAGATCCCCAAGGTGGCTCTCGTATCCAGAAA
WI-1245a	85	T	C	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTCAAGCCTCATAAGGAAGGAGTAGGTGTTAATGGCA TCCTAGGCAATGGTAGG[T/C]CTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAATTCATTTATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCTCGTATCCAGAAA
WI-1031	149	G	A	---	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTTCCCAACCCTGGCACCAATGACAGTTTGGACCAAA TAACTCTTGTTTCAGGGGACTGTCCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACACAACACCCCTCCCCAACAATCATGACAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCCTGATTGAGAACCACTGGTT
WI-5385	110	G	A	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAACAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGCGGGAAACATTGAATGCA
WI-5403	199	T	G	---	ACCAAACCGTTGGCAAAGGCTCCCAAGACTCACCACACCCAACTTGGTGCTTGCTTACCCTATGCGGGGTG GGATTGAAGAGAAATAACCATAAAATATAATTTCCAGTAGTTACCAGGCACCAGCCTAT TGGAAGAAATCATAAATGTAACCCTACAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGT[T/G]GGCCTACAACCCATTTATCATTGAACCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G	A	---	TGGTATTTTTCCTTTCCTAAAAATGTTATGATTAATTAGTGTCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAGAAAATAAAGTATAGTTGAAACCTCTAAACAATTTTAGATTTTAAGGCCTAG GGAAAGAAGAGAGCCTGGGAA[G/A]GGGAATGAGAAAAGCACAACCAGAAAAAAAAGTGTGT GGCTTAAGGGGAAGGCCAAGGAAAGTTAAGT

Marker	Pos	A1	A2	Sequence
WI-5801a	48	A	G	TGGTATTTTTCCTTTCCTAAAAATGTTATGATGATTAATTAGTGTCTTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTAGATTTTTAAGGCC TAGGGAAGAAAGAAAGAGAGCCTGGGAAGAGAGGAATGAGAAAAGCACAACCAGAAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT
WI-5696	61	C	A	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCCACACCGAGGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCTCTGTATTA TACAAACTGGGACCAAAGATGACTTTATAATAGTGGCAAGGACAATCAGGCAGACTGGGAGGACC TTATAAATAGATTATAAGGCTGTGGTGAGTTTATTTTAACTT
WI-7461	153	C	T	TATTACTAGGTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCCC AATTCTTAACGCTCCTCCACTTCCCTTCGAACCCAGCCTCAGGATGACCACTTAGGCTGCACATTCCTG TGGGCAGGGACTGTGTC[C/T]GTTCCCGTTGGGTCCCGGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTGAGCATGTGCTGCA
WI-9716	221	G	A	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTGGTATACTTTCTCTTTCTGAAGACCAACCCCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTTGTACTTCCTACATTCTGGAAAACTAAGTGAGTTAGGCTCTCTTCATCT CAATTGAAAATTCTAGAA[G/A]AAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C	T	TTTTCGTTAAGTCTTGTGAAGCCACACAGAAGTGATCTACTCTCTTAC[C/T]AAGTGTTACTTTGCA TATATTTATGGGATGATTCTATCCCTCCTTACTTAAGATTTTCTCTCTCAGGTTAAATATTCCATTTCCT TTGTTCAGGAGTTTCTTATTGGCCTTCTTATTTTGGTGTGAGGTTGTGAGGTTGCTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A	C	GAAAACCTCGTTGGCTCAAAGGAAACTGTAG[A/C]AAATTCTTTTTTTTATTTTGTTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGACGCGTGCTCTTTGTTTGGTGTAAATCCTCTAGT GGGCACTTTGCAAAGCAATTTAGAGCAAAGGTGGTGGCATGGTGGTGTGAGGTTGCTGAAAG TAGCAAATGGAAGAAAAGTTAATGGA
WI-10312	41	A	G	AAGGCCCAGTGGGAAAAGCAGACAAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCATCA GTAGAGATGGGATGCCTAGGAGGTCATGCTAGTGAGGGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAAGAAAATTTCA
WI-11152	179	C	T	GATTCTTTGCGACATGCAGAGCAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCCGCACCAGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA[C/T]CTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

ID	Pos				Sequence
WI-1968	167	A	G	...	TGGTGAGGAGCTGTAAGGCTGAAAGAATAGTCTCTGCTGCTCTGGTCTTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCCTCTTGCCATGGGTGTTATGTTTAGAATCATGGAAGTTGGAAGACTTAGAATTCA ATTTGGGGCTGTACAGTTACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGTCTCTTAAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G	A	...	GGGTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCCTCCCCACTCTA CCCGCCAAGTCTACCTTTGGTTCTTTATTTCTGCTAATGACCCATACTATTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164	C	A	...	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCATTTAATTA TGCACTTACTTGTTGGCTACCAGACATTGCTTCCAATTGTAAATTCCTAACAACAGCAAGCATAACT GATGTGTCCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCCTCTGT CTTCCTCTGTTCACCTCCTGTATTCCCTATTCAGCATTCAATGATTA
WI-4860	72	A	G	...	AAAAAAACAACTTCATTTGACATTCTAAGAAGATAAAGAAAACAACAACAACGATCCACTGTGTGTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAATTAAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGAAAGCCAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGAGCATTAATATAGCA
WI-9705	111	C	A	...	TGAAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAAGTAAATCGGAAGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTAAGGAGTTCGGCTGCC[C/A]AAAATTGTTAACACTGATGC TGTCTACAAAGCACACATAGAAATCGGTGGTAGATTGCGGTTCCTAGTAAGTAGCTAAGTGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
TIGR-A004248	177	A	G	...	CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGATGATTCATGTAAGGGTGGGCAGGGTGGACTG AAGAGATCGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGGAGAATCGTGGGGTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGTCTTCATACGCCACAGA[A/G]TCCTCCAATTTCAGGGGCTCCC GTGGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T	G	...	GGGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCCAGAGACAGAATAGACCTGGCCCCTTCCTTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACGCCAGCTCCCCATGCCAAATAGAACGATGAGTGCTGGGATCCAATTTCTATGGGAGCC TGGGGAGAGGGGATCCTTTCTAGTTGA
WI-7747b	88	T	G	...	GTGAGAGCGAGGCGAGCCTACAGATGAACTCTTTCGTTCGTTAACTGTTGTGTATGTACATA TATATATTTTTAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCCTTGTTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCCATTTGTAATAAAGTATATAATTTTTTATGTTTTGTTTCTGA

Marker	Position	Allele 1	Allele 2	Sequence
WI-7747a	44	T	C	GTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTGGCCTGC[T/C][T/C]TTCGTTAACTGTGTATGTACATATATATATTTTTAATTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTTATTTCTTGTTTGTTTGTTGGGTATCCTGCCCAGTGTTGTGTTGTAATAAGAGATTTGGAGCACTCTGAGTTTACCCATTTGTAATAAAGTATATAATTTTTATGTTTGTTTCTGA
WI-7189	197	T	C	TCCAGAATTTCCTTCTTCAGCTCATTTGTCTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGTCACATACCACCATTATTTCCCCTTCAAACAAATAATTTACAGAAGCAGGAGCAAAATATGGCCTTTCTTCTAAGAGATATAAATGTTCACTAAATGTGGTTATTTTATTATTAAGCCTACAACATTTTT[T/C]AGTTTGCAAAATAGAACTAATACTGGTGAAAATTACCTAAAACCTTGGTTATT
WI-7850	57	G	A	AGCCCCAGCTGGACTCATGGATGTGCACCCTTTGCTCCCTGCTCTTTCTGCCTCTGG[G/A]CTCATGTATCTGCGCAGCTCTGGTACCCTCTGTGGGTGCCATCTCTACCCTGACACAGACTGCCTGCCTGAAGCTGAGAAGGCACAGGGCCAAGGAGCCAAGGACCACAGAGCCTCAGCCAGCCCAGGATCCGTCCTCATTTATTGGTGATGATGAATGGGAATCAGGGGGCTGTGTCTACTAGAGCC
WI-7907	69	G	C	CTCTTCTCTTCATCCCATCACCCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGGG[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTTTAAGAAACATTGTTTGGTGGCAGCAATCTCCCTGTCCCTATCAAGGTAAAATTATTGTCAAAGTTTAAATAGCAAGTCAAAACTTGGATGTATCATCAAGGTAAAATTATTGTCAAAGTTTAAAT
WI-7919	242	T	C	GAAGGCAGCTGGATCACTTCCCGCAGTCCTTGGGCAGCCGTTTGCTGTGTGGAACACGAGAGCTCCTCCTCAGGGGCCTGGCCACTCCACCTTCCTTCTGTATGATGTATTTGGTTAAACACTGTCAAATAATAGAGATGTGCCCAGAATTTAGATTTTCTTACCCTAATCTGTTTAATATTGTTAATTGTAACTTTATTCCATTTGAAAGTGTCAAGCCCATTCAGATAAGCTATAAATCTGGTCTTTAAGGAA[T/C]ACAACTTT
WI-7928	101	T	G	CTCCCTTCCTATGTCTCTCAGCAGCGTTGGGGCACTGTTCATCTTCTGACCGTTTGCTCTGGGCTATTCCCCTGCAGTGCAGACATCGTCAAAATTCA[T/G]ACAAGAGGAAATTTCATGCAGAAAAGCTGTATGCAGGATGCTCACTGATGTTTTGCACTTTAAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTCTATCTCCATCTCCTCATTAAAAAATACGTACATTTCGAGGTAATGGTA
WI-7936	131	T	A	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATTATATACATCTTGGTTATTTCTGAAGGTAGCATTCTTTGGAGTTAAAAATGCACATATAGACACATACACCCAAACACTTACCACCAAAC[T/A]ACTGAATGAAGAAGTATTTTGGTAACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATGCAGAAATAGACAAAAAGTATATTAAACAAAGTTCAGAGTAATATTGTTGAA
WI-7944	99	T	C	TACACGTTCCAGCCCGTTGCCCCACTCATCTGCCGCCTTCGCGCTTTCATG[T/C]AGCCCAAAGTACAGCCTGACCCCTGGTGTGAATGCTTTCCATCTCCAGGAGACTTTCATGTGTAGCTAGTAAGATTACCCTGAGCTGCAGCCTGAGCCAATGGCAGTATATTGTTGACAGACAAAGATGTGGGAGATTGGAGCATTGAAACTAAGAGCTCTCAAGTCA

Marker	Pos			Sequence
WI-7805	101	A	G	TTTCTAGGCTGTACAGTCGTGATGCATGATTTTTTATAAATATTTCATACTCTTGTGAATTTGGATCTT TTTACTTTGAGCAGCATATATTTAGAATATGTGTA[A/G]TGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTCATTGTGATGGAATAGTTTAACAGTCAGGAAATGAAAAATAAATGAAGTAT CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137	G	T	GGCCAGGAGGATTAGCAACAAGGATTCATTCTGTTACTTACTTGCCCCTTTTATCTTTCCCTCTTGCCC CAGTGCCCTTCTCTCCAGTCTCCAGGCTTCATGTGAAGCTCTGCACAGACAGACACTCAGTGTCCTGGCAGTGCT [G/T]CTACTCCTCCTCAGGTGCAGCATACACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAAGCAACACTCAAAAATTGGCAAATGTCATCAG
WI-140	252	C	T	ATTTGAAGATTTGGAGGGCTTTGCAGAGGAAAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTCAGCCCAGCTCATTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTTAAAAATGTGTCATTTGTCTGTATTGGCATTCCTTC/ GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTGCTGGCACC CATGATGGAAACTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCATTCCATCCTGACTTTAAAA TTCTAAACAGCCTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C/T]GTTTAACAAAGCATAGAATATTCTGAACAACT
WI-198	218	C	T	TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTG[T/C]CCAAAGGCTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205c	146	T	C	TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTG[T/C]CCAAAGGCTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205b	146	T	C	GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCAAGTNCTTCCAAGAGGTCTCAGACTACCTACCTCTCCATCTCCCCCT CTCCCCCACAACACAACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTGGTGCTTTAGTTTTCTCAAATGGGAAATGG
WI-234	165	G	C	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTGACTCTCTTATCCTCTTCTTATCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCTGCCTGAACGACCCCTGCCTGCCTGAAAGACCTCTCTGAAAGACATGGGGCGGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCCCTGAAAGACCTCTCTGAAAGACATGAGTAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTATCCCTGATGACTCCCGGGCAAA
WI-276b	25	A	G	

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WI-276	25	A	G	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCTGTGGCTGCCTGAACGGAGGAAGGATGGGGCGGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCTGCCTGAAAGACCTCTCTGATGACTGGGCAAA
WI-427	59	G	A	TCTGGCAAGGGCTTTGTCTTATCCTCCCTTGCTATCCGTAGATTTAGAACTACTTCC[G/A]GTTT TTTTCCCAATCCACAGGTAAAACTAATAATAATGGATGTATAGAACATTTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTCCCTGGGGAAAATATTCACAAAACATTTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGTCTTGCTCTGTCGTCACCCAGCTTTCAGTGCAGT
WI-562c	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA[T/C]AAATGGTCCTTTTATTAAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA[T/C]AAATGGTCCTTTTATTAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTT[T/C]AATAAATAATTCTCAGGTAATTATGGCCACAGCCAGTCT AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141	A	G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATGAGTCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A	G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATGAGTCTCTGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A	G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGTAATGACCCTCCATGAGTCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

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WI-611	66	G	C	TTCAAATTTAAACACCATTGGGTATATTATATAATTTTNGCTCTATCCATAGTTCTAACCCTCTTCTCT[G/C]ACAGTGGAGACACCTGCCTTCTATTGTCCTTGACGTATTAACGTATTCGATCAGTCAGTCACCATCTGGAACCAAGGTTCATTCTGCTGACCCTCCTCCTCCGCCTTCCTCGCTTGGGCTCCAATACGAACCTTCTCTGTGTGGCGTCCGCCTTCCTCTCGCTTGGGCTCCAATAC
WI-681b	156	A	G	TGAAGCCCTCTCTCTATACCCAAGTGTCTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAAATTGTTATAGCTATT[A/G]TTATACTATGGCAACCATTGGGACACAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
WI-681	156	A	G	TGAAGCCCTCTCTCTATACCCAAGTGTCTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAAATTGTTATAGCTATT[A/G]TTATACTATGGCAACCATTGGGACACAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
WI-867b	119	G	A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTCCATCTCC[G/A]TTTGTGTGTTTGGCCAAATAATAATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGGTTGAATGTGTCCCCCACAAAGCACATTAGAAACTTA
WI-867	113	A	G	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTC[A/G]TCTCCGTTTGTGTGTTTGGCCAAATAATAATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGGTTGAATGTGTCCCCCACAAAGCACATTAGAAACTTA
WI-867	119	G	A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTCCATCTCC[G/A]TTTGTGTGTTTGGCCAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAAACTTA
WI-871b	123	C	G	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACACAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGAATGATAAGAGCACCACCTACCTCATG[C/G]AACTGTTGAGAGAAATAAATGAGACATTGTAATGTAAAGTTGTGTATGGCCTGAATTGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA
WI-871	123	C	G	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACACAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGAATGATAAGAGCACCACCTACCTCATG[C/G]AACTGTTGAGAGAAATAAATGAGACATTGTAATGTAAAGTTGTGTATGGCCTGAATTGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA

Name	Pos.			Sequence
WI-884	198	T	C	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCCTTATTAGGAACTTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAAATCCACCTCATTAATCATGACAACNNAAAGGAATA[T/C]G ATCCCGCCATGCAACATTTATTCAGTGAAAAATGAAAATGAACATAAT
WI-921b	205	G	A	CACTTCCCAAGGGCTCTCGGGGANGAGCGGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGAGGTGCACACGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAGTCTTNGCCAGGAAAAAGCACGATCCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-921	205	G	A	CACTTCCCAAGGGCTCTCGGGGANGAGCGGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGAGGTGCACACGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAGTCTTNGCCAGGAAAAAGCACGATCCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-945c	90	G	C	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGATCATGACAGATTTTCTTGGCTTTA
WI-945b	90	G	C	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGATCATGACAGATTTTCTTGGCTTTA
WI-960b	167	C	T	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTC[C/T]CTTAGAGGTATAAGTCATATAGGCAATATTCT ATGTATACTAAAGGTGTATGGCATAAGAGTACATA
WI-960a	155	G	A	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T	C	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGTGCCTAGGTACATTTGTTTTTATTTGTTCTG CGAATTGTTGTTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCTTTCTGTGTTC CTTCTTAAAGATACAAAATAACAAATAAATGTAACATTAGACCTCTCACTA[T/C]CGCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTTTATTGCTGGCTTCATTTGTAAATNTG

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WI-1147b	204	G	A	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCACATAGGCATATGATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACTTCTCCTCTCCTGCTGCTCCTGAGCCAAAAACAGGCATTACCATAAATCACTTGTTAGGATGAACTTATCTGGCCAAACTGATAC[G/A]GCATGACCCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C	T	GCATTCAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTCTATGTCAGGCCCTTGGTGTTGAAGACGCAATCATGACAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTGTCAGGTGCGGCCAGGTTAAGTGCTGGGG[C/T]TTCTGGGGTCAGGTCAGGCTGCCTGGGTCCATCCTGGCTCCAAACTGCTTTGCTATGGCT
WI-1158a	124	C	G	GCATTCAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTTGAAGACGCAATCATGACAACAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGTGGCTAAGTGCTGGGGGTCTGGGGTCAGGTCAGGCTGCCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATGGCT
WI-1304	124	T	C	AAGTTTACAGAAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCATCATCTTCAANGTNCCCACAGCACTTATCCCCTAGACAGCCATTCTTTTGAATGNT[C/G]NCANTAAAAATGATTTGAAATTGGGAATAAAGCCCCTCCCTATTTTATTTCTTCTTTATTTCTTCCATTCTATGTTGGTAAATATAAAGATGGGC
WI-1305d	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTCTTTATTTCTTCCATTC[C/T]ATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACATCCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATGTGCAGGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTCTTTATTTCTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACATCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATGTGCAGGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTCTTTATTTCTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACATCCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATGTGCAGGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTCTTTATTTCTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACATCCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C/T]AGGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A	G	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTAGAAGCCATAGAAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTGTGAAGGCCAGTTGAAATTTATCTTCCT[A/G]GC
WI-1306	240	A	G	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTAGAAGCCATAGAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTGTGAAGGCCAGTTGAAATTT[A/G]TCTTCCTAGC
WI-1307b	118	T	C	---	GACAAGGCTGGTACTAGTTTCCAAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGTTGGGGGAGCCAGTGGTGTGTAGGCCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T	C	---	GACAAGGCTGGTACTAGTTTCCAAATTCCATATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGTTGGGGGAGCAGTGGTGTAGGCCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T	C	---	GAGAGATGGCCAAGACAAAGCAGAGGAGAAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACACATGGAGAC ATTCATTAGGCAACTACAACATGTGCCTTGCTC[T/C]ACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGAATTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C	T	---	GAGAGATGGCCAAGACAAAGCAGAGGAGAAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACACATGGAGAC ATTCATTAGGCAACTACAACATGTGCCTTGCTC[T/C]ACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGAATTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T	C	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACAACTATGGAGCTGAGAGTCTG[T/C]GAAGTTGGGTAGCTACCAGGCCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C	G	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACAACTATGGAGCTGTGAGAGTCTGTGAAGTTGGGTAG[C/G]TACCAGGCCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

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WI-1341b	136	G	A	TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGTNTGCNNNTCCTTTTCTNTTT ACCTGATCCACTATCTCTCTCAAGATCANGTTCAAATTTGGCTTNCTTTGTTNAATTATACCCAAGC [G/A]GGATTGTGATGGATCTGTTTATTTCCTGTGTCTTGGAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349d	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349c	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349b	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1403b	57	C	T	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTGGTAAGTTG[C/T]TTCCGAAT GCCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGCCCTGCCATCATGCAITTGGCAATATGTCACATAGCTGTCCTCA TAATCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT
WI-1403	58	T	C	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTGGTAAGTTGCT[T/C]TCGAA TGCCCACTTTATAAAGTTAGAGGTTATACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG AAAGTTTACATCAACATAATTCTTGCCCTGCCATCATGCAITTGGCAATATGTCACATAGCTGTCCTC ATAATCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT

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WI-1417c	31	C	T	CAGGCCCGGAAGAGAGATTCACGGTGGAGAGAGATGT[C/T]TTGGCCCAGGAGGGGCGGGGGCAGAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCAGTTTGGAGGGGGCTCGGCTTCAAAAAGCTGGGGTCCGGTTTTGAGGCGGGTTGC AGGCGAGGCCCTTAGGTCGCGTATTTAATGTTTGCTTGTAGAAAAAGTCGC
WI-1417b	31	C	T	CAGGCCCGGAAGAGAGATTCACGGTGGAGAGAGATGT[C/T]TTGGCCCAGGAGGGGCGGGGGCAGAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCAGTTTGGAGGGGGCTCGGCTTCAAAAAGCTGGGGTCCGGTTTTGAGGCGGGTTGC AGGCGAGGCCCTTAGGTCGCGTATTTAATGTTTGCTTGTAGAAAAAGTCGC
WI-1729	172	A		CCATGAGCAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCCATGTATATCTGTATTCTT TTTATTCTCTCCAAAAGAAATTTCATTATGCAAAACATTATCAGGCAATGCAAGCTCGTGTAATAAAGA TGTTGGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGTCCTTCCGTGGTNACCTTCTCTCCCACCATCACCTGTGTTTT
WI-1732b	122	T	C	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCCTT[T/C]ATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C	T	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGT[C/T]AACCCTTTATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGAGTGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97	A	G	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTAAAATCTGTGTTGGA CATAATGTTGAATTTGCAGTTCACCTTGG[A/G]TTTAAGGTGTGCTGTTTTCTGGCAAAGAGTCAG TGGGAGTGTCCGGGAAAAAGGGCTAAAGTCTTTGTAGTCAGACAAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31	A	G	GGTACACAAAGAAAATGCTTCTGGAAATCTAC[A/G]TAGCGCCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAAACAAATAATTCTCATAGTTTACACAACTCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAAACAAATAATTCTCATAGTTTACACACTCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTTGAGTACAGAGGACATTCAAGAATAATCATAAAAAT
WI-1803c	77	A	G	CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATCTTACTAAAGCATGACTTCTAGAAAATTACTTACTTATTCTTGTCCTCAA GGAAATGGGAATACCTATAATAATACAGTCTTATTGGAGGAAAATAACTGGAATCA

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WI-1803b	77	A	G	CCACTCAGTAATAATAGTAGTGTTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAACCATTATGAT[A/G]AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTGGGTGCTAATTTCAAATATATCTACTAAACAGTCTTATTGAGGAAATAACTGGAATCA
WI-1837b	112	C	T	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTTGATAATTCACTTCTTTTCCCAGGCTCAAGGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1837	112	C	T	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTTGATAATTCACTTCTTTTCCCAGGCTCAAGGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1840b	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTATATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1840	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTATATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1879b	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTTCTTTCATAACTTACTCCCCCCGCACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTA[C/T]GTCTGCNAAATAAACTCCCAAAAAAGTGGTTAGTCCAACAGGGTTTTAATAGTTCTTGTTGAATTTCTGTGTGCGACCCGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTTCTTTCATAACTTACTCCCCCCGCACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTA[C/T]GTCTGCNAAATAAACTCCCAAAAAAGTGGTTAGTCCAACAGGGTTTTAATAGTTCTTGTTGAATTTCTGTGTGCGACCCGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119	C	T	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCCNGCTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGTAAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCTGACTTCAGATCTGTGTGCTTAACTGCCATGAAGAGAAACCACTTTCTTTGCTCC

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WI-1900	119	C	T	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGAACCACTTTCTTTGCCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGGAAAGACCAGCC[C/T]CTCTGAAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGGAAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGGAAAGACCAGCGC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCACTGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A	T	CCAGGTGAGGCTGAAAGAAGGAGGAGGCAATTGCTGTTGGAGGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A	T	CCAGGTGAGGCTGAAAGAAGGAGGAGGCAATTGCTGTTGGAGGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T	C	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTTGTTTTAGTCTGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCCTACTGCGTCTGTGTGAAAGCCTTTCCCCATCGAGTGATACAGTACTTTCCAGTTATGGGAGATTT[T /C]TAACAATCAAACACTGGCTGAGGCTGTTGG
WI-2012	102	T	C	AAATTCTAGAAGCCAGAAGTCAGCTCACGATTTATAAAGTGAAGTAAATGCATTGTAGTTTCATGT TTTCTTCTTAATTCTGCACAAAACTAGCTAAAAATCT[T/C]TTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTCTACTCTCATT GGCTTCACCCAATGCTTCCACTGGATC

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WI-2013	127	C/T	CTTTTAGAGGTGGTCATTCGGTTCCCTTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGACAGATAAATGCTGATACTGACACT[C/T]CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGGATATCTCAGCTTTCTGAGCCCCTGGTTACTGCAATCC
WI-2032c	166	G/A	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTTCTTNACTTACTCATATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACAC[G/A]TGGGACCTCGTCTCAACCTCCGACTTTCAC AGATCATTGGTTAGGCTCACCTTCCTGTAATTGCTCTGTTTTTCAAAGGG
WI-2032b	219	C/G	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTTCTTNACTTACTCATATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACGTGGGACCTCGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTCTGTTTTTCAAAGGG
WI-2032	219	C/G	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTTCTTNACTTACTCATATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACGTGGGACCTCGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTCTGTTTTTCAAAGGG
WI-2054b	188	C/T	CGTTTCTTCTACACATCTTGGGGNACATAAAGAGAAGNAGCTGTCTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGC[C/T]TCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGATGGGCTGTCTT
WI-2054	183	T/C	CGTTTCTTCTACACATCTTGGGGNACATAAAGAGAAGNAGCTGTCTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGC[T/C]GTTCCTCCTGCCTGTCTCTTT CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGATGGGCTGTGTCTTT
WI-2573d	129	T/C	TGGGATTAAAACCCTGTTTCTTCCTCCCAGTTCAGTGTGCCTTAATGTTGTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTCATCATATGGCTGGGGCTTGGACGAG GAAGTGAAATGATTTGCTTGCACAAGGTCATCATATGGCTGGGGCTTGGACGAG
WI-2573c	165	A/C	TGGGATTAAAACCCTGTTTCTTCCTCCCAGTTCAGTGTGCCTTAATGTTGTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTCATATGGCTGGGGCTTGGACGAG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGGCTTGGACGAG

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WI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCAACCAGGGCTTATTTATGCCTAGGTAAGGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT CATCTGATCTTCCAACCAGGGCTTATT[A/C]TGCCTAGGTAAGGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A	C	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT CATCTGATCTTCCAACCAGGGCTTATT[A/C]TGCCTAGGTAAGGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T	C	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCAACCAGGGCTTATTTATGCCTAGGTAAGGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A	G	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTACAGACATTAAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCCACTTAAAGAGGTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A	G	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTACAGACATTAAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCCACTTAAAGAGGTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T	C	CATGCTGTGTAACCTCTGTGCTGCTTGTGCTGTGTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCATTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT
WI-2870	131	T	C	CATGCTGTGTAACCTCTGTGCTGCTTGTGCTGTGTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCATTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT

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WI-2954c	49	T A	TTAGCACACATATCTGTTGTGGGACTTAAACTGAGACAAGGCATAAAAAT[T/A]CAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41	A G	TTAGCACACATATCTGTTGTGGGACTTAAACTGAGACAAGGC[A/G]TAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTGGCCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38	G T	TTAGCACACATATCTGTTGTGGGACTTAAACTGAGACAA[G/T]GCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTGGCCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62	T C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGTAACCTCCTCCCTCCTTAATAAACCTAAC ATTTCCTTGTTCCCCTGACATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT AGTTCTTTAATGTGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2971	62	T C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTAACCTCCTCCCTCCTTAATAAACCTAAC ATTTCCTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGTCCCAGATTGCAATCCT AGTTCTTTAATGTGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTA /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTA /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGAGACAGAACTAGCAGAAAGTGTT

			Sequence
WI-2995c	151	G C	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTT[A /T]AAATCTTTCTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAGAAAGTGTT
WI-2995c	151	G C	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C	TTCCTGGGAAAGAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTT[A /T]AAATCTTTCTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T	GTGGTGGTGCAGTTCATCCTCCCTGTGAGATCCAGAGACTGGAGCGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCTTACTCCTCCTGAGACTTCTTCCT GAATGAATTACACTGCACTCAATCCCTGCCTCAGTCTCTGCTTNAGGGAACTTGACCTAAGACAGAA ATCTTAGTACCAAATACTTTGCAAGG
WI-3147	85	C T	ATTCTGTATAGTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGACAACAACAGAAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACCATCCTTAATAAGCATATCAAAAATTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTNATATCTTAT
WI-3234b	68	T C	ATTCTGTAATGTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGACAACAACAGAAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACCATCCTTAATAAGCATATCAAAAATTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTNATATCTTAT
WI-3234	68	T C	ATTCTGTAATGTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGACAACAACAGAAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACCATCCTTAATAAGCATATCAAAAATTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTNATATCTTAT

WI-3292b	106	G	A	GTTTTGCTAGAACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATTGGATTGGGGATGGATTACTT GCCATGAAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATATTNCCATGA GACACAAATGGAAAAATGGAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3292	106	G	A	GTTTTGCTAGAACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATTGGATTGGGGATGGATTACTT GCCATGAAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATATTNCCATGA GACACAAATGGAAAAATGGAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3355	19	G	C	CCATGAACCATGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCCAAGCACTTAAAACTCATCAGAA AAAAAAATCATCAAAAAGTCGAAGTTAGTTTTNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATTATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G	A	CCATGAAGAATGAGTTCCTCCTCCCCTGGGTCACGTCTAAGAATAGCACACCCTTGAGAATTTNACT TAGCACGTGGCATTGTAATGGCTGAAGTTCCTCCGCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAATTGGGATGAAATCTNACATTCAATGTGCACCCTCGTGTGGGATCCACTTCTCC[G/A]TGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGG
WI-3505b	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATTATTT GAAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAACAAGANANANGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3505	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATTATTT GAAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACAGCAAGAAAAAAANGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C	T	GCTAGTAAGGTTCCACCTAAAGTGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACCAAGTGTTTGTGGTGTCATC AGTGTCACACACATGCTACCTTCCTTCACAAAACAAA
WI-3564	177	C	T	GCTAGTAAGGTTCCACCTAAAGTGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACCAAGTGTTTGTGGTGTCATC AGTGTCACACACATGCTACCTTCCTTCACAAAACAAA

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WI-3649	64	A	G	AATGTCCATGCTGTGACTGACCTGTCTCTAACACCTTCCTAGTATTCCTTTAGTGGAAGATTCAC[A/G]AGACCAGTTTGCCTTCACTTAGTAGGGCCAATGATAGACTTTAGGTGCTACCAAGGGTACCTGCACAGCCACATCATATGTCACAGTATGGTTGCAAAGGACCTGTCTCTAGACTCTTTCTGCCTGCCTTGGTCTTCCTGTTTTACCATATTAAATGACGACATGCAAACCTCAGAGCCTTTTA
WI-3674b	133	G	C	ACAGTACACACTGGCCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTTAGAAAATAACAAAAT[G/C]AAGAAAAAAATGATAGTAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G	C	ACAGTACACACTGGCCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTTAGAAAATAACAAAAT[G/C]AAGAAAAAAATGATAGTAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G	A	CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTTATTGGCTCTCTTCTCTCTCTCTTTAATGCTCTCCAACACCAATTCACTTTATTCTTTCAAT[G/A]AGCATTTGTCCAATTAAAGTCAATTAAAATAATGTACATTTTCAACAAGTATACACATTAAGCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACACTGAGGCTTCTGATTAATAACTCTGGTTCAGGAGAAGGCAAGGGCAGTATGACCACTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAATGGCCTGTCCCACTCCACAGAAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACACTGAGGCTTCTGATTAATAACTCTGGTTCAGGAGAAGGCAAGGGCAGTTATGACCACTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAATGGCCTGTCCCACTCCACAGAAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G	A	AGCCAGCCACATCATGTTGAGTCCTGCCATCTTCCATCTTCTTTATTTCTCTCTACTGCCTTCACCTTCCATTAACAAGAACTCTTGATTACATTGTATGTTGGTTACACTACAGAATCCAAGATGACCTCCCCATCTCAAGGTCAACTAATTAACACCTTAACCTTTGTCAATCTTTGTCATTACCATAACATATTCATGG[G/A][T]CTGGGATAAGGGGTAGACATTTTTATGGGAGGCATTA
WI-4110b	130	T	C	GAAAAATGATGTTTTGATTTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCTTCCTCTCCTCGTTATTTGCC[T/C]ACAGTTTAGGTAAATAACAACTCTGTTATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGGGTAGGGGACAAGTNCAGAAAAGGGAGGAGGGTNGGGGGGTTTTCTGGGAAGA

WI-4110	130	T	C	GAAAAATGATGTTTTGATTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAAACTGATAGT AACCTTTATTTGATGAAACTTCTCCTTCTTATTTGCCT[T/C]ACA GTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAAGTACAGTAAAAGTAGCAACCATGGG GTAGGGACAAGTN CAGAAAAGGGAGGGAGGTN GGGGGTTTTCTGGGAAGA
WI-4119b	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCGAAGTGTCCAGCAAGGGCTTGGGTGGGAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAAACAGGACAAGAACAGAGAAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4119	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCGAAGTGTCCAGCAAGGGCTTGGGTGGGAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAAACAGGACAAGAACAGAGAAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4123b	51	G		CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAAATTAGTGGGG TTCTTCCATTGACATTGGCTTGTTCTTCTCCAACAGTGGGTGGTTTGGATGTTTCCTATGCTTCTC AGGCACACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAAACAATTTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAAATTAGTGGGG TTCTTCCATTGACATTGGCTTGTTCTTCTCCAACAGTGGGTGGTTTGGATGTTTCCTATGCTTCTC AGGCACACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G	C	TTGTACATGTTCATTCATCCCTCCCCATTCTTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACTGTAGT AGGAGAGACAAGACAAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T	C	TTGTACATGTTCATTCATCCCTCCCCATTCTTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[T/C]GTGCTGTGCCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACTGTAG TAGGAGAGACAAGACAAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G	A	TAACACACTTTCATTGGTTTCCTATTACTGCAGTAAAAGGACCATCCATTATATTACAATTCCCTC AGTTCTATGCTTTAGAGTNCTATTATAGGACTACTGTAAAATTTCAGAGGGAATTACTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACACATGCCAATTGCACAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCCTTCCCAAGTTCTTAAATTCCTAG

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WI-4230	93	T	AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTAGTTTAACATTTGATAAGAAATTGATGAAA GTTTGTCACATTCCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTAAATGTAATTCTGAAT ACATTTAAATGGAGGAGAATGAATAGTGACCTTTGAAATTTGAAATTTATGG
WI-4241	118	C T	GAAAATTCCATTGAAGTTTTGACCTTGAACTGATCTCATTAATACTTTTNCTTGTAGTGGTTGTATTT CATTTTGACAACAGAACAGACGAAAATTTCCACTTAAAATTAAAATTCTC[C/T]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAAAACTGTGAAAATTATCTCCTAGAATCTTCAGAATCTAGGATGGAAG AA
WI-4271b	151	A	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAAGATCAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGGAATATTAGAGTNCTACAGGGAGCCCCCAACCCTCCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151	A	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAAGATCAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGGAATATTAGAGTNCTACAGGGAGCCCCCAACCCTCCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156	G A	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTATGTATATTTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGGATGAACCTGAGGAAGAGAATAGAAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAAATGGAACAGACATGATTGACTTA AGAGGTATTGTGTAGGAACTGGAAGCGGTAA
WI-4389	156	G A	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTATGTATATTTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGGATGAACCTGAGGAAGAGAATAGAAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAAATGGAACAGACATGATTGACTTA AGAGGTATTGTGTAGGAACTGGAAGCGGTAA
WI-4488	31	A G	GATGACAATTATTGTGTATTGGCATTTAAA[A/G]GTACCATTCCATTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTTAGTCGTATTGCTCCTTTCTAGTTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAAATGCTCAG
WI-4491	145	G C	ACCATCAATGTATCCACCTTCTAAAATTTATTAGTGATGATTAACTGGCTCTGTTAAAAAATAAAAACCT GTCTTGGACATTGAAAATAAAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAATCATAAAAATGCATAAAAATCATAAAAATTTCTACCACTGTCA TTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A	G	TTGGTTGGCATTTAGCCTCATAACAACTATTTACAATCATAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAAATGTTAATTAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAAATAGGTGTGCTTTAATTGTTTATCAGTATGC
WI-4639	185	C	T	TTTCTGCATTGAATGTGTATGGTCAGACTTCAGAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGAGATCTCAGTTTAACTTCCAATTCCACCATTTAC TGACCCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCATCAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A	-	AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGAGA[A/-]GATTACTCATAAAAGCATATTAATTTTATAAAATATGAAAATTTAACTAGATAATTAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGGGAGGAGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGTACAGTCGTTCTAAGCAGACAG
WI-5390	87	C	T	GCTTTGAGAATGAAAAGGGAGGAGCCTGGACCATTGCAGGGCCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTAT[C/T]GTCTGTCTCCCCCTTGGTATGCTGTCTGTGTCATGAAACAATGAATTC CCCAGTCGCCTGCGCCGATTCGTGGCCGATTCCTAGAGGTGTCCAGAAAAAAGTTCGGTGAATAGAATTG ACGAATGGGTTCAGAATTGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G	A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTATAAGCAGT GCAAACATTATTTAATTT[G/A]AAAGAAACTTGTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5404	87	G	A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAACATTATTTAATTT[G/A]AAAGAAACTTGTTCTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5545b	77	A	C	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTATTTCATTTCA
WI-5545	77	A	C	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTATTTCATTTCA

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WI-5860b	134	A	G	ACTCAAGTTGGGGGGATAAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGT TTCTTTTTATATAAAATTATGGATTTGTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATCGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A	G	ACTCAAGTTGGGGGGATAAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGT TTCTTTTTATATAAAATTATGGATTTGTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATCGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C	G	GCAAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCACAATAC TATATATTGTCCTGTTCTGAATTATTTCATTTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGCTTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATT[C/G]ATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAA AAACCCTATATTNCTTGTGCTACTTAAAATGTATAATGTGGGAGAGAAGGAATTTGATG GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAA ACCCTATATTNCTGT[T/C]CTTGTGCTACTTAAAATGTATAATGTGGGAGAGAAGGAATTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAGAAGGAATTTGATG ACCCTATATTNCTGT[T/C]CTTGTGCTACTTAAAATGTATAATGTGGGAGAGAAGGAATTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAGAAGGAATTTGATG AAACCCTATATTNCTGTGCTACTTAAAATGTATAATGTGGGAGAGAAGGAATTTGATG GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96	T	C	AATGCCTATCACCTTCCATCGTGCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[T/C]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTTGACTAAAACATACTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T	C	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAAGGAAGAAGAGAATATTCCTTTCTTTAGTGATTGCTTAATATTAATTCATAATAAGTGCACCATCTCTT[T/C]GCTCCTTATAAATGTGTTAGAAGAAGGAAAATTGAGTGTTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTTCCTATTTTCTTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C	T	CTGGCCCTTATAATCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTTGTCTACAAGATTCCTCCTCCAGTAGGGCTTGGGTGTTGGCACCGTTGGCTCATTC[C/T]ACTCTCCCTGGGTCTTATTGACTTCAGGGAGCCTAGAAGAGCTTAGAGAAACCTGCTTCTTTGCAGAAAGAGTCGGGGTTCCAAAGAATTCGTTACGATTTTTA
WI-6336b	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCCATATATTCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAACAAACTAAACAGCTTATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTGGTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6336	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCCATATATTCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAACAAACTAAACAGCTTATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTGGTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6381	92	C	A	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGTATTTATACAATTACAAAAATGGNTTCATGTTTAACAA[C/A]GTATTTAAAAGTCAAACATTTTAAAACAGGCACAATATTCTAAGGCATATGCATTCACCATGGCTTTGAATGTCCCACTTCACAACTCACAATCACAAAATCTACAGANGCGGCAAAAGATCAGAGTTCAG
WI-6436	198	C	G	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTAGGAAAAGAGAAGTTCAGAGGCAAAGTCATGACAGACAGAGGAGAAATACAAGGCTTGGTGGTTGGTTGTTGTAGTGGTTAGTAGTAGGTAGCGTT[C/G]ATTTTGGGTGTATTCCACAGACAAGGTGATGTTCTAAGGTGTCTAAGATTTGATATTATTGT
WI-6449	186	C	T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGTGTATGGCTAGTGTTGTTGTCTATTCATCTGCATTCATCTGCATTCGTATCTGGTTCATCTCTGCATTCTCTGCGTCTTATGTCTGGCTCTATT[C/T]ATCCCCTATTCTCTGATCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGTGGTGTATTTATA
WI-6449	186	C	T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGTGTATGGCTAGTGTTGTTGTCTATTCATCTGCATTCATCTGCATTCGTATCTGGTTCATCTCTGCATTCTCTGCGTCTTATGTCTGGCTCTATT[C/T]ATCCCCTATTCTCTGATTCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGTGGTGTATTTATA

WI-6463	72	T	C	GCTGGAGAGAAAAGACCTCCAAAAGAAGAAACTAAATCAGAGTCTCTTGAGCAGAGAGAGGAATTGAAA AGAACA[T/C]TGAAAAAATTAAAGTAGAACTCAAAAGTCCCAATTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCCGCATGCTG
WI-6474b	76	C	T	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C	T	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T	A	GAACTCAATTAACTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCAAATGGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCAGCTCCTCGTAGGACCTAGAGACCTAGCACACAACTG
WI-6478	175	T	A	GAACTCAATTAACTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCAAATGGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCAGCTCCTCGTAGGACCTAGAGACCTAGCACAACTG
WI-6559	149	G	A	CACATTTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAAACATGCAAAACATAAGGCAACAATTCTGATCATTTTATAGGNTCCCAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTAAAAAGAGAACAGGAAATAAGGAAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G	A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54	G	A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA

WI-6608b	46	C		CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGGAGGGGGGATTCCTCCTAGTCCTCTCCCTAGAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACTCCCAGCACTAG GTAAAACTGCAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
WI-6608	46	C		CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCTCCTAGTCCTCTCCCTAGAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACTCCCAGCACTAG GTAAAACTGCAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
WI-6666	68	C	A	GTTAGACAGTATCCAGCAAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCC A[C/A]AAATCCCATCAACAACAGTCAGTCAGTCATCATGCTGGAAGCATTCTGTCTTACTCTGTTGGTTCATGTAA ATGTTTGGGGTGACTCATTCCGCCTCTTCTNTCTCAAGTTCCAGCCTTCTTGGGTAGACCAAAACTA ATACACAATGTTAGAGCACACAGAGA
WI-6670b	120	A	G	AGATTAACACATAATTATATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAGAAGTTGAGACAATGAAC[A/G]TTGTTAGCCA GCCATTGCCATTCAGGGCCGGAGTCAGGGTTTGTGGGGCCCAGGAATTTGGGGAATTCTGA AAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120	A	G	AGATTAACACATAATTATATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAGAAGTTGAGACAATGAAC[A/G]TTGTTAGCCA GCCATTGCCATTCAGGGCCGGAGTCAGGGTTTGTGGGGCCCAGGAATTTGGGGAATTCTGA AAAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCGATCAGCAGTGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCGATCAGCAGTGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCGATCAGCAGTGAAGAGTCTAGTACAAGATAGGCAGACATG

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WI-6710	106	G	A	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAAACACATTTTGTCAGGCTGGAATGATTCCC[G/A]TAGTAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTGAGACCTTCCTTGGACAGGAGGGTC
WI-6766b	148	G	C	AAAACAAATGGTGCATTGCATATATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148	G	C	AAAACAAATGGTGCATTGCATATATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6787b	97	A	G	ACAGATAAAAGTCTTTATTCCCCTGTATGTTTACATAAGAAAGTTCTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTCAC[A/G]TTTTACTGACATATCTTCATGTGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT GAGTGCAATAGGGCAGGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105	C	G	GAACCCACCAGGTCCTGTTATTTATTAAGGAGGCATTTACATTTATGATAGCAAGTTCAACACATTCA TCAACAAGGCGGTCTTCAAATCAATCAGTCAACCCC[C/G]GAGTTAGAAAGTAGTCATGAGGAA GAGCTGCTTGGCTGTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCCGGAAAGGGCAGGACTGAAGCCA GAGCCCAGANTCCTGGCAATTCCAGTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T	C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCGAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T	C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCGAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C	A	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAATCCAGTTGTAATCAGATACCCTGTGTGCTCTACTNGCCTCCAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG

Marker	Pos.	Allele 1	Allele 2	Sequence
WI-6817	145	C	A	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT TTGCTTTTTGTAATCCAGTTAAGACCATCAGACCATATAGATGGATACCCTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGGATCATCA GCAGGGTAAC[C/A]TGTGGATACCCTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG
WI-6819b	221	C	---	GATGGAAAGCCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACACATTTGCATATACAAAAATTTCTGCTATTTG CTTTAGCAAACAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G	T	GATGGAAAGCCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATT TTGCTTTAGCAAACAGCAATAACTTTGTGTTTCCTATATGACACCTAATAT
WI-6826b	154	A	G	GCAAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAAATAC ATGCAAAAACCTTGTACATTA[A/G]GAGCTTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGGTATACGTTG
WI-6826	154	A	G	GCAAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAAATAC ATGCAAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGGTATACGTTG
WI-6857a	122	T	C	AGTGCAAACTATTTTGAACAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAAATACAGCAGATGAGATGTCTCCACATGTA[T/C]ATTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGTAATTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G	A	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTTAAAATCTAAACAACAACAGCTTG TTTGTGGTTCGTCCTGAAATCCTCCCTGCTCACAAAACCAGCTACTNGGTTTTCTAAAAGACGTA ATTTTGCAGGCAAACTTC[G/A]TATGAGAGCCATTCTGTGCAGAAGAAAGGGAAGGGAGGAAGCTGTTGTT TTACCTGTAGTATGAAGATATTCTTTGCGCTGTTAGAACTGAGCTCATTAA
WI-6909	73	C	T	ATTGAAAACTGGTTAGCAACAGAATAAATTACAACATAAGAGCCTGATATAAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTTTGAAATCAGATTTTATGATAC GGAAAAAAAATTTCCTTTTTGCCAACAGGATTATTTCGAATAATAAATCTGCCAGTGCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163	G T	CACTCAAAAACCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCATATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCATGGCTCTTACACTTAAGCCATTCATTAAGCCATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAAGTCAGAGTGGCTGACCAGTCCCGGACCTCCATGTGAATGACTCTTCCTGGC
WI-6915	144	A -	GCTTGTTTTTTGTTTGTTTTTTTAAGTGACACCTTGGCCTTGTGGGCATTCTTCCTTCACTTATCTTACCCAAAAGTGCCTTTGGGCCCAGCCACTGATTTAAAACCCAGAAATGTGGTTTAAACAATGTGGTCGTGGGTGAATTCAGGTGATTTTNATTTTCTATTTGGTAGTATTTTCAGAATTTTCCCACAAAGAACATGTATTGTCTTTGTAATTTGAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACTCTGTCACACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTTCATGTCCCATGCTTTGTCTTGGTCCCTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGGTATCCTGGCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACTCTGTCACACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTTCATGTCCCATGCTTTGTCTTGGTCCCTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGGTATCCTGGCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAAATTCCCTAGGTAAGATATCAAGTTACAAANTACAAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6955	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAAATTCCCTAGGTAAGATATCAAGTTACAAANTACAAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6957	47	C G	AAACTAAAAACCCTTATTGTCTCCAAGTGTGTGGCAAAATAGAAAATC[C/G]TTTCAATTACATTAGGAAATCGGGTGGATAACGGAGTAGTTATTCCACTTAAGAAGCATTCCAGTCAAATAATCACAAAACAAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAAAACCACTTTAGGCTAAAAATAAATGTATATGAATAATGCATAGACTGTGTATCTGAAAAATCATGC
WI-6996c	242	G T	ACTTCTAGTGCCTCTGTTACCACTCACCACCTCAATGCCTCTGGTCCGCCGCACCTCTGATGTCCGTAGGCCTTAAATCTGCCTGGCGTCCCGTCCCCTCTGTCTTCAGCACCCAAGGCTCAGTCCCTGCTGGACCCCAGCCGGCAGTTCCCTGCAGGAGAGGAGGGGCTGCTGGACCCCTGTCCCCGTCCTGACTCTCCTCCTGATGGTGGGCCCTGTGGGCCCTCTGTCTCTTCTTCC[G/T]GTCGGATC

Name	Pos	Alleles	Sequence
WI-6996b	242	G T	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCTCTGTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTGTCTCAGCACCCAGGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAGTCCCTGCTCTCAGGACCCCGTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGCTCTCTTCCG[G/T]GTCGGATC
WI-6996	228	T G	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCTCTGTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTGTCTCAGCACCCAGGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAGTCCCTGCTCTCAGGACCCCGTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTG[T/G]CTCTCTTCCGGTCGGATC
WI-7021b	112	G A	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAAT[G/A]CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCC[A/G]AATGCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCGCAGCCTCCTCCACCTCCATGACAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCGCAGCCTCCTCCACCTCCATGACAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	AATTCGGCTGAAAAAGGAACTACCTATCCTTACATTTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT[A/C]TCTTCTTTTTTATCATTTATCAGCCTTTATGTGTATTTCCAAGTAAAAATATTA ACATATTATTTCATTGGTCTTCTTTTTTATCTGGTTCTATATGAATGCTAT
WI-7091	153	A C	AATTCGGCTGAAAAAGGAACTACCTATCCTTACATTTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT[A/C]TCTTCTTTTTTATCATTTATCAGCCTTTATGTGTATTTCCAAGTAAAAATATTA ACATATTATTTCATTGGTCTTCTTTTTTATCTGGTTCTATATGAATGCTAT

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WI-7136	58	T	C	TGTGAAGCCACATTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACTG[T/C]AATTC TCTCAATAACTCAGTGTAGCACTTAAAGTCTGAAGGACGCAACATGAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGGTTGGCTTTTTAATTTATTTTCTTCATCTTTATAACAAGAAAGNNNNN NNNNNNNNNNNNNNNNNNNGTAGCTTTCTATATATG
WI-7146c	210	A	G	GGGACGCCCTGTTGTTTGGCTCAATTTGTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCTGTCTCTCCTTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCCAACATGGATGTGTTGCCCCTCCTCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210	A	G	GGGACGCCCTGTTGTTTGGCTCAATTTGTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCTGTCTCTCCTTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCCAACATGGATGTGTTGCCCCTCCTCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202	G	A	GGGACGCCCTGTTGTTTGGCTCAATTTGGGTTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCTGTCTCTCCTTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCCAACTGCGAACTGGAGAGAAAATA [CCAACGCAGTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATA
WI-7153	161	A	T	ATATTACAACTTGCTTTTAGCTGATCTCCAAATGACTCTTTTTCTTTATATGTTAACATA TATAAAATGCAACTGATAGTCAATTTGATTTTATTCAGGAACTATCTGAAATCTGCTCGAGAGCCT ATGTGCATAGATAGATGAAACNNNNNNNNN[A/T]AAAAAAGTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATTGTAAATGGTATGTT
WI-7155	156	T	G	TAGAATAGATGCGGTCATATTCTTCTTGGCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAACACCACCGCTGGCCTACCCCTATAATGATCCTGTGTCCTAAATTAATATACAC CAGTGGTTCCTCCTCCGTGT[T/G]TAAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTCTAG TCTCACTCTCTTGTCCCACCCTTCTCTCCCAACTCCAG
WI-7169b	161	A	G	AGCTCCACCAGATGCAGATTTGTGTTTTGTTTTCTTGTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAATACAGTTGTCTAGCCAAGCCATCAAGTGTCGAAATTCAATATTGGTTTATGCAAAT ACAGCAAACTTTATTTAAGTAGAT[A/G]GGAGAATATATGTTAAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTCTCAAATGAAGTGTTATATATA
WI-7175b	194	C	T	CTCCTAGACTAGTGCTTACCTTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAAATATATAATGTTTACTGCTGTCATTGTCCATGCCTA[C/T]AGAT AATTTATTTGTATTTTGAATAAAAACATTGTACATTCCTAGTACTGGG

ID	Pos			Sequence
WI-7175	194	C	T	CTCCTAGACTAGTGCTTTACCTTTATTAATGAACTGTGACAGGAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAGAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAATATATAATGTTTACTGCTGTCATTGTCCATGCCTA[C/T]AGAT AATTTATTTTGTATTTTGAATAAAAAACATTGTACATTCCTGATACTGGG
WI-7178b	273	G	A	TGTATCAGGTCAGGGACTTGGACAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCCGCTGTCACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7178	273	G	A	TGTATCAGGTCAGGGACTTGGACAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCCGCTGTCACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116	A	C	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTATTCACCAGTTCCTCTGCAACCCACTCTGAGCCTA[A/C]TCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106	C	A	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTTATTCACCAGTTCCTCTGCAACCCA[C/A]TCTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7191b	273	T	A	ATAATTGCTTGTTTTCTCAGCCTGGCAAGATATTTTCATAAAAGAGGGATAAACAATGCTGATTACTAC CTTTTAAAATATTTTAGATAAATGCACAGCACCACCAGCACCATCTAAGCACATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTTAAGCACTCTAGAAAACAATGAAGCTTCTTGGCATATTTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATTGTAACTCAGCAAGTAGAAGACCATTT
WI-7199c	112	T	C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCCGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCCTTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTGGTGCTCTGAATTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
WI-7199b	112	T	C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCCGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCCTTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTGGTGCTCTGAATTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA

WI-7216c	237	T	C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTCCTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCACGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTT[T/C]CTTGTAATCACTT
WI-7216b	237	T	C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTCCTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTT[T/C]CTTGTAATCACTT
WI-7220b	147	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTA AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTAGTGTGTT
WI-7220	140	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGGC[A/T]CTAGAAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTA AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTAGTGTGTT
WI-7226	232	C		GATCGAATTTTTCAGATGATTCGGAAATTTCATTCAGGTATTTGTAATAGTGACATATATATGTATA TACATATCACCTCCTATTCTCTTAAATGTTAAAATGTTAACTGGCAGTAAGTCTTTTTGATCATT CCCTTTCCATATAGGAAACATAATTTGAAGTGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACTTAACGATTCTTACGATTCTTCTTCGGGGTTT
WI-7228b	254	G	A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTTGTCTTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGT[
WI-7228a	163	G	A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTTGTCTTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAA[G/A]ATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213	C	T	CGATCGTACTGCCAGTAGCATTGTCTGTCGTCCGGTCTTGTTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTCTAGGAAGTCAAAAAAATATAA TAAAGGGTTGAGCCCTCACTTTCTTCTTGCCACCTTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG

				Sequence
WI-7233b	213	C	T	CGATCGTACTGCCAGTAGCATTGTCTGTCGGTCTGTTGTACATTCCATTTCAATTGTTACAGATGTGAACTTTATTCCTTGTCACTACTTTCTTCTTGCCACCTTTTTGTGGCAATATTAAAGTGAACTGCTAATATAAAGGGTTGAGCCCTCTACTTTCTTCTTGCCAAAACCACTGCCAGATAACCAGAGGGGCCTG
WI-7233	211	T	C	CGATCGTACTGCCAGTAGCATTGTCTGTCGGTCTGTTGTACATTCCATTTCAATTGTTACAGATGTGAACTTTATTCCTTGTCACTACTTTCTTCTTGCCACCTTTTTGTGGCAATATTAAAGTGAACTGCTAATATAAAGGGTTGAGCCCTCTACTTTCTTCTTGCCAAAACCACTGCCAGATAACCAGAGGGCCTGGTGTAAGT[T/C]ACGTGCACAAAACCACTGCCAGATAATCGTGTATCTGTAAACACTTTTGTTCTTAGTCTTTTCTG
WI-7238	128	T	C	TAAAATTGATGTTCTTTAAAATCGTTAATGTATAAACAGGGCTTATGTTTCAGTTTGTTTT[T/C]CCGTTCTGTTTTAAACAGAAAAATAAAAGGAGTGTAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGTATGCAGTAATTAGAACAAAGAAGAAACAATTCAGTAGAACATTTATTGCCTA
WI-7252f	520	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCAGACGCCGGGACAGAGGCCTGCCCGGCGGCCGCCAGCCCCCGGCCTCGGAGGCTCGGTCTCGGTCCGGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252e	552	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGACAGAGGCCTGCCCGGCGGCCGCCAGCCCCCGGCCTCGGAGGCTGCCCTGGGGCTGGGGCGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252d	540	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGACAGAGGCCTGCCCGGCGGCCGCCAGCCCCCGGCCTCGGAGGCTGCCCTGGGGCTGGGGCGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAGAGATGGGAGCTCCTCTCCTGGAGGATGCCCTGGGGCTGGGGCGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252c	552	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGACAGAGGCCTGCCCGGCGGCCGCCAGCCCCCGGCCTCGGAGGCGTTTCTAGCAAGTGAGAGATGGGAGGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252b	540	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGACAGAGGCCTGCCCGGCGGCCGCCAGCCCCCGGCCTCGGAGGCGTTTCTAGCAAGTGAGAGATGGGAGGACACTCCTAGAGAACGCAGCCCTAGAGCCGTTTCTAGCAAGTGAACTCAGTCATTAGACTCCTCCTCCA

WI-7252a	520	T	C	CCACCAGGATCCCAGCCCCAGGCGGCCCCTTCCCACTGCGAGCAGCAGCGCGGGACAGAG GCCTGCCCGGCGCGGCGCGCCGCCCCGGCCCTCGGGAGCCTCGGGAGGCTGCCCTGCGGCCCCTGTTCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTTCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTATTTGCCACCAAAAAGTCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTT[T/A]AGGAGTAAAGATTTGCCT
WI-7265l	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTA TTTCCAGTATGTGTTATTTGCCACCAAAAAGTCATTTCACCCATTCTG[T/G]GGTTCATTGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTT[T/A]AGGAGTAAAGATTTGCCT
WI-7265k	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGT[T/A]TATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTT[T/A]AGGAGTAAAGATTTGCCT
WI-7265j	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTT[T/C]AGGAGTAAAGATTTGCCT
WI-7265i	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTT[T/C]CTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGT[T/A]TATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGATT[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT

WI-7265f	231	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTGTATTTTTCTT[T/A]AGGAGTAAAGATTTGCCT AAAAATACCACAGTTTGTATTTTTCTT[T/A]AGGAGTAAAGATTTGCCT
WI-7265e	227	T	C	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTTTATTTATGTAAAATATAACGATCT AAAAATACCACAGTTTGTATTTT[T/C]TTAAGGAGTAAAGATTTGCCT
WI-7265d	174	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTTTGT[T/A]TATTATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7265c	170	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATT[T/G]TGTTTATTATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7265b	121	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGT[T/G]GGTTCATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7265a	80	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTT[T/A]TATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7281b	183	C		---	GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCCAGTGTCGCCCAGCCTGCCCTGGCAAAAACGGAGTCCGCAGGCCA CCCCATGGTCTGATGGGCATGGCATCTCAGACTCT[C/A]TTGGGGGTCCTGCAAGAAGGCCTCCTC GTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCAAGAAGGCCTCCTC
WI-7281	171	C	A	---	GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCCAGTGTCGCCCAGCCTGCCCTGCAAAAACGGAGTCCGCAGGCCA CCCCATGGTCTGATGGGCATGGCATCTCAGACTC[C/A]TTGGCAAAAAACGGAGTCCGCAGGCCG CAGGTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCAAGAAGGCCT

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WI-7282b	159	G	C	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCACTCAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTTCATAAAAACCAAACT[G/C]TAGCAAGATGCAAATGCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTCACCAAGACAGTGCTGAGATTGG
WI-7292	92	T	C	CTTGATTACTTCCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCACTCCACTAC TCTCTTCCTCCACTTCATTTTCC[T/C][T/C]TGTCCTTCTCTAATTCAGTGTTTGGAGGCCTGACTTG GGGACAACGTATTATTGATATTATTGTCTGTTTCCTTCTTCCCAATAGAAGAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGTGGTGGAACTATGATGGTTACAATGAAGGAGGAAATTTTG[A/G]CGGTAGTAACTATGGTGGTGGTGGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAATTATGGACACATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7301e	94	T	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG[T/G]T[G/G]TGGTGGTGGGACTATGGTTACAATGAAGGAGGAAATT TGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7301d	138	A	G	AACTATGGCAGTGGTCCTCGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGTGGTGGGACTATGATGGTTACAATGAAGGAGGAAATTTTGA CGGT[A/G]GTAACTATGGTGGTGGTGGGGGCAGTTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7301c	211	A	C	AACTATGGCAGTGGTCCTCGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7301b	182	C	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGGAACTATAATGATTTTGGAAATTA[C/T]AGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7301	88	G	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGTG[G/T]CGGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACTATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG

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WI-7301	205	A	C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGTAGAGAGGCGGGTATGGTGGTGGTGGACCAGGAGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGTGGTGAGAAGCTCGGGCAG AATT[A/C]T[GGACACATGAAAGGGGGGCAGTTT[GGTGGGAAGCTCGGGCAG
WI-7314c	49	G	A	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTTAATTTGGGAGGTCA[G/A]T]TGTTCTACCTCACTG AGAGGGAACAGAAGGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGTGGGTCCTTTCTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAAACTTGTTTTT
WI-7314b	49	G	A	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTTA[A/G]TTTGGGAGGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTCTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGTGGGTCCTTTCTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAAACTTGTTTTT
WI-7314	36	A	G	ACTCAGGGAAGGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAGTCCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAGNNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGCTGGGGTGTGCAGCCACATCCAAGACTGGAGCCACAGGCTGGCCA
WI-7321b	199	C	T	ACTCAGGGAAGGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAGTCCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAGNNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGCTGGGGTGTGCAGCCACATCCAAGACTGGAGCCACAGGCTGGCCA
WI-7321	199	C	T	AGACATTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCTACCTACTATAGGTCCAGAAGTCCTTATGTTAAGCCCTGGCAG GCAGGTGTTGTTATTAAAAATTCTGAATTTTGGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7336b	248	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTCACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGTCAGAGAACAAAAGAAACAGAATCAATATATAATTCAAGACTATCTGCAGCTA
WI-7338c	221	A	G	GTGTGTTCTTCTTTACACACAC[A/G]TATACACACAGAGACATCAGAAAATTCTGTT

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WI-7338b	125	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATGATGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCTTCTTTACACACATATACACACACAGACATCAGAAAATTCTGTT CTAGTGTGTT
WI-7338	125	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATGATGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCTTCTTTACACACATATACACACACAGACATCAGAAAATTCTGTT CTAGTGTGTTTCTTCTTTACACACATATACACAGACATCAGAAAATTCTGTT
WI-7338	221	A	G	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACACTGCCAATGATGAGGTGCAAAGAATCAATATAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTTACACAC[A/G]TATACACAGACATCAGAAAATTCTGTT
WI-7384c	146	T	A	CCTATGTCAATGAAATGCTAGGGGGCCAGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAATACATTGTATTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTT[T/A]AAAAATTCTTAATGATTATTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGGAAATTTGAGCAGAATTTAAAAAGAA
WI-7384b	146	T	A	CCTATGTCAATGAAATGCTAGGGGGCCAGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAATACATTGTATTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTT[T/A]AAAAATTCTTAATGATTATTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGGAAATTTGAGCAGAATTTAAAAAGAA
WI-7384	145	T	A	CCTATGTCAATGAAATGCTAGGGGGCCAGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAATACATTGTATTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTT[T/A]AAAAATTCTTAATGATTATTTATTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGGAAATTTGAGCAGAATTTAAAAAGAA
WI-7388c	106	A	T	TGAAATCCTGGGTCTCTTGGCCCTGTCCTGTAGCCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]AAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTTCCCCAAAGATGTGTATAGTTATTGG
WI-7388b	106	A	T	TGAAATCCTGGGTCTCTTGGCCCTGTCCTGTAGCCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]AAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTTCCCCAAAGATGTGTATAGTTATTGG

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WI-7388	94	T	A	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTGAGCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTATCAAGAAG[T/A]CTGAAGCGACTACTAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7438	64	A	G	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCGAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAAACCCTATTGGAACCAAGTCTTCAGATTGTNCCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTACCA
WI-7454b	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCGTGTGGATGGTACCAACAACAACAAGCCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT[T/C]TGTTGTTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCGTGTGGATGGTACCAACAACAACAAGCCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT[T/C]TGTTGTTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177	G	C	AATTTGAAAATCTGAAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464b	168	C	A	AATTTGAAAATCTGAAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464a	103	C	A	AATTTGAAAATCTGAAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTCCTAT GTACACAGAGCCACAGCCACAAGAGGGTGGGCATAAGCAGTTGCCAGCAGTTGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7499b	134	T	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCCAGACAAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTGAATGCTTCA[T /G]TATAGTCCTCTTCATTAGCAATCAGTGAGCAATCAGTGAGCCATCTGGCATCATGTCATCCCTTTTTTTAGGA ACTCTGTACAAATTCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

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WI-7499a	33	A	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAA[A/G]CCATTCCAGAGACAAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCCTCTTCATTTAGCCAGTGAGGCAATCAGTGAGGCAATCACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAATTCCCTTTGAAATATAAATTTTGGAAATGAGTGATGA
WI-7506b	118	A	C	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAAAGTAGTCCTGGTGCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A	C	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAAAGTAGTCCTGGTGCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C	T	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTTGCGGGTTTCTTGCGGGTTCTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAATTTTCTTTAAATTATGGTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7534	135	T	C	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTTGCGGGTTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGC[T /C]AAATTGTCGTGAAATAGGTTAGAATTTTCTTTAAATTATGGTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7543b	162	G	A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGCTGAAGGAATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGAATTGCATGCTTCCTCCTTT[G/A]GGAAGACCAGCTTTGACGTCCTTCCTGGATGTAGTCAGTTA CTCTGCAGCCCTCAGATTATTTTCCTCTGGCCGTCCTTGGATGTAGTCAGTTA
WI-7543	162	G	A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCCTTT[G/A]GGAAGACCAGCTTTGCAGTGACGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCCTCTGGCCGTCCTTGGATGTAGTCAGTTA
WI-7555c	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAAGAAAGTGGTATGTTGTGTGATAAAATGAAGTCTGACACTTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAATGAAAGTCTGACTAGAAATTCTATTGCAGAAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCATTTGAATTTCAG

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WI-7555b	60	T	C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAGAAAGTGGTATGTGTGATGATCAGCATCAAGTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGTACATTTAGT ATGGCCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG
WI-7555	60	T	C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAGAAAGTGGTATGTGTGATGATCAGCATCAAGTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGTACATTTAGT ATGGCCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG
WI-7567b	290	G	T	---	TGAGCCATCACTAGAAGAAAAGCCCATTTCAACTGCTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGGAGACAGGGTAGGGAAAGGGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCTTGG ATCGCCTAAGCTGGCTCTGTTTGATGCTATTTATGCAAGTTAGGGTGTCATGTATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCTTGGATCGCTCAAGCTGGCTCTGTT AATGTATCCCCTTTCGGTCCAACACAGGAAACCTGACTGGGGCAGTGAAGGAAGGGGATGGCA[T/C] AGCGTTATGTGTAAAAAACAAGTATCTGTATGACAACCGGGATCGTGTTGCAAGTAACTGAATCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCCTTGGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATGCCTACCGAGAGGAAGAAGGAGTTTG
WI-7569b	63	T	C	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTTGTGTTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTTAATCCCTCTACAGTGAGTCCACTACCCTACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGCAAGCAGCCCTGACCCAAGGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGTGAGGAGGT
WI-7574c	216	A	G	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTTGTGTTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTTAATCCCTCTACAGTGAGTCCACTACCCTACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGCAAGCAGCCCTGACCCAAGGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGTGAGGAGGT
WI-7574b	216	A	G	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTTGTGTTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTTAATCCCTCTACAGTGAGTCCACTACCCTACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGCAAGCAGCCCTGACCCAAGGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGTGAGGAGGT
WI-7574	216	A	G	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTTGTGTTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGCAAGCAGCCCTGACCCAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGTGAGGAGGT
WI-7576c	168	A	T	---	AATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTCACCTAC TTTGTAAGTGAGAGAGACAAGAAGCAAGAAACATAAGAAAAATAAAC

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WI-7576b	168	A	T	AATGATGATGATGATGACGACGACGACGATGATGCTTGTAACAAGAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTGGAAGTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTCACCTAC TTTGTAAGTGAGAGAGAGCAAGAGAAGCAAGANNNNNNNNNAAAGAAAAAAATAAAC
WI-7577q	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577p	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAA[G/C]TGTTTGCTTTCCTTTAA TAAAATATGCATCAAATCGTCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577o	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAATATGCATCAAATCGTCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577n	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577m	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577l	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577k	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC

WI-7577j	117	A	G	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577i	77	T	C	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577h	50	G	C	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTAATAA AGAAGTTCATTTGGTTACAC[G/A]TAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577g	157	G	A	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577f	48	A	G	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577e	84	G	A	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577d	93	T	C	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577c	154	C	A	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAGAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC

WI-7577b	117	A G	---	AACCATGTTCCCTCTTCTTAGCACCACCAAATAATCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A	---	AACCATGTTCCCTCTTCTTAGCACCACCAAATAATCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAG[G/A]GTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619q	106	C G	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACT[C/G]TCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619p	150	T C	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCCT[T/C]CTAAGGGAAACATACACAGAAACATACCGAGAAACCTATTTC TCTCGCTTTCTTTCTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619o	228	A G	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATA[A/G]CACATACCGAGAAACCTATTTC
WI-7619n	237	G C	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAA[C/T]GAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATA[G/C]AGAAACCTATTTC
WI-7619m	99	C T	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAA[C/T]GAGACTCTCTGTGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619l	189	T A	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACCGAGAAACCTATTTC

WI-7619k	90	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCC[C/G]TCCCTAAGCGAGACTCTGTGCTGTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACGAGAAACCTATTTC
WI-7619j	206	T	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTAAGCGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTCCTCT CGC[T/G]TCTTTCTTACACAGAAACATACACGAGAAACCTATTTC
WI-7619i	106	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACT[C/G]TCTGTGCTGTGGGGGTGCTAATTACTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACGAGAAACCTATTTC
WI-7619h	150	T	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCCTAAGCGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCTCTC CAGGAAGAATGGGGCCT[T/C]CTAAGGGGAGTGTGGGGCCTGTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACGAGAAACCTATTTC
WI-7619g	228	A	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTAAGCGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTCTTACACAGAAACATA[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTAAGCGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTCTTACACAGAAACATACACATACC[G/C]AGAAACCTATTTC
WI-7619e	99	C	T	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTAAG[C/T]GAGACTCTGTGCTGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T	A	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCAAGAC AGAGAAGGGCCAATGGGTCATCCCCTAAGCGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCAT[T/A]CTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

			Sequence
WI-7619c	90	C G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGGCCAATGGGGGTCATCC[C/G]CTCCCTAAGGACTCTCGTGCTGTCTCCCTTTTTCCATCTTTTTCCT ATGGCAGGAAGAATGGGGGCCCTCAAGGGAGTGTGGGGTCTCGTGTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACTACCGAGAAACCTATTTC
WI-7619b	206	T G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGGCCAATGGGGGTCATCCCCCTCCCTAAGGACTCTCGTGCTGTCTCCCTTTTTCCATCTTTTTCCTCT CAGGAAGAATGGGGGCCCTCTAAGGGAGTGTGGGGTCTCGTGTCTCCCTTTTTCCATCTTTTTCCTCT CGC[T/G]TTCTTCTTACACAGAAACATACACTACCGAGAAACCTATTTC
WI-7619	189	T A	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGGCCAATGGGGGTCATCCCCCTCCCTAAGGACTCTCGTGCTGTCTCCCTTTTTCCATCTTACATGG CAGGAAGAATGGGGGCCCTCTAAGGGAGTGTGGGGTCTCGTGTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACTACCGAGAAACCTATTTC
WI-7626d	105	A G	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626c	155	C T	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTGCCA TACTAATGATGAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626b	28	T A	CCTTTGTATGTGGAAGTATACCTGGCTT[T/A]TTAAAATATATGTATTTAAAAACAAAAGCAACAG TAATCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626	144	T C	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTGCCA TACTAATGA[T/C]GAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7689c	134	A G	TCCCATAACCGGCTGCTGATTCTCAGGGTCTCTGCGCCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGCCCAGACCTTCTAGGACGCCACCCAGCAAAGGTTGTTCCTAAA[A /G]TAAGGGCCAGAGTCACACTGGGCACTGGGGCAGCTGTGATACAAATTGCAGTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAAAATGGATTTATTAGAATTTCATATGAC

WI-7689b	134	A G	TCCCATAACCGCTGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGGCCAGGCCCTTCTAGGACGCCACCCAGATGGGGGAAAGCACAGGTGGGC /GTAAGGGCAGAGTCACACTGGGGCAGTCGATCAAATTGCAACAAATTATTAGAATTCATATGAC
WI-7689	121	G A	TCCCATAACCGCTGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCCAGTGGCTGGCTGCTGCCCAGGCCCTTCTAGGACGCCACCCAGCAAAA[G/A]GTTGTTCCTAA AATAAGGGCAGAGTCACACTGGGGCAGTCGATACAAATTGCACAAATTCATATGAC GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G A	TGGAGAACATTCAATCTTGCCGTCACTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAGCACATGGTAGTGCAAAGAGAGGTCCAGAGTCCTGGCCCCTTGAT GCCCAGCTCAGTGCCACAAAGCTCAGTGAGGGGATGTTCCAGTGGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
WI-7703b	164	T C	ACAGAAAAGTTGAATTTACATGGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAATTTGGTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGTCTATAAACCAAACTGATGT[T/C]AAGTAAATGGTCTCTCACTTGTTTATTTAACCTCTAAATTCT TTCATTTTAGGGGTAGCATTTGTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C	TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGGAAGACTGTTGCTGGCCACTTGGAGCCAAGG GTTCAGAGAGTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGCCCAGCCAGCTCTCAGCC GAGGGGCAGAACAGCGCGCTCCTGCTCTGCCCAGCCAGCTCTCAGCC
WI-7743e	106	C A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGCTGGCCACTTGGAGCCAAGG GTTCAGAGAGTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGCGCCCTCATCCGAGGCAGGGTCAGGA GGGGGCAGAACAGCGCGCTCCTGCTCTGCCCAGCCAGCTCTCAGCCAACG
WI-7743d	275	C T	TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGGAAGACTGTTGGCTGCCACTTGGAGCCAAGG GTTCAGAGAGTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGCGCCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCGCTCCTGTCTGCGGCCACTGGGGGTCCTGCCCAGCCAGCTCTCAGCC
WI-7743e	106	C A	

				Sequence
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGCCTCGGGGGTCCTGGGCCAGCAGCTCTCAGCCAACG TACAGAATTCTGCTACCTCACTGGGGTCCTGTCTCTGCCAGCAGCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC
WI-7743e	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGCCTCGGGGGTCCTGGGCCAGCAGCTCTCAGCCAACG GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGCTCGCCAGCAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GAGGGGCAGAACAGCCGCTCCTGTCTCGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACT GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGCTCGCCAGCAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GAGGGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC
WI-7743c	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTACT TACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCAGCAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGTCTCTGCCAGCAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC
WI-7743	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTACT GTGTACAGAATTCTGCTACAGAATTCTGCTACCTCACTGGGGTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GAGGGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGAGACTGTGGCTGCTGGTCCTGGTAATAAGTACTGTG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGCCTCATCCGAGCAGGGTCAGGAGAG TACAGAATTCTGCTACCTCACTGGGGTCCTGTCTCTGCCAGCAGCCGCTCCTGTCTCTGCCAGCAGCCAGCTCTCAGCC GGGCAGAACAGCCGCTCCTGTCTCTGCCAGCAGCC[A/G]TAGTTTAAACATTTCC
WI-7758	144	A	G	TGACATTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCTGTTAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGAACATCAAGTG GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAATTTATAACAGAATTAAAGTAGATTTTAAAA GATAAAAATGTGTAATTTTGTTTATATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G	C	ACAGGGCCTTTGGCAGGTGCAGCCCCACTGCCTTTGACCTGCCTCCCTCATGCATGGAAATTCCCT TCATCTGGAACCATCAGAGAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TAGG GAAAACATTCCATCCTTGAGTCAAAAATCTCAATTCTTCCCTATCTTTGCCACCCTCATGCTGTGTG ACTCAAACCAAATCACTGAACTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C	G	TTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTT GATAAAGATTTTCCTATTCCTTGGTTCTGTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAAGGCA GACTAGGGTTCATGTTCATGTTGTTTTACCCTTTNNNNNNNNNTTGTAAAAGTCTAGTTACCTACTTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T	C	TGCAACCTCTTTTGTGATGGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGAACGGCACCCAGAAT CAGATCCCAGCTTCGGGCATTTGATCAGACCAAACAGTGCTGTTTCCCGGGGAGGAAACACTTTTTAA TTACCCTTTTGCAGGCACCACCTTAATCTGTTT[T/C]ATACCTTGCTTATTAAATGAGCGACTTAAA ATGATTGAAAATAAATGCTGTCCTTTAGTAGCAAGTAAAATGTGTCTTGCT
WI-7785c	165	G		GCAGAGACCTTCCAAGGACCATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNTGTATTTATTTTGTAAATGTATCTTGGTGCTGC TAATTTATTTGTCCATTGATGTATTTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165	G		GCAGAGACCTTCCAAGGACCATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTATTATTATCACATTACCA ACATTGGTCATTGTGAATANNNNNNNNNTGTATTTATTTTGTAAATGTATCTTGGTGCTGC TAATTTATTTGTCCATTGATGTATTTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785	156	-	T	GCAGAGACCTTCCAAGGACCATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATANN[- /T]NNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCATAATTTATTTTGTCCATTGA ACATTGGTCATTGTGAATANN[/T]NNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCATAATTTATTTTGTCCATTGGTG TGTATTTATTTTGTAAATGTATCTTGGTG
WI-7789c	84	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAGGAGGGGCACCATCTCTTACAGAGACTCCC TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTCGGTGACTCGGCGGGCGTGTCTCAGACGACCCAGGACCATCT
WI-7789b	84	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAGGAGGGGCACCATCTCTTACAGAGACTCCC TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTCGGTGACTCGGCGGGGCGTGTCTCAGACGACCCAGGACCATCT

WI-7789	73	G A ---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAAGTCTCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAATGTGACGACTACTCTCAGGCCCGCTGCCCTAGGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGCCCAGGACCCATCT
WI-7790b	190	C T ---	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T ---	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A ---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTCTTTCTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTTAATGATTAAAATAGCATGCCCTTCTCTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81	C A ---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTCTTTCTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTTAATGATTAAAATAGCATGCCCTTCTCTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G A ---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTTCCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814b	41	G A ---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTTCCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814	28	G A ---	TTCTCTCTCATTTTATCCCTCACCTGTA[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTTCCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA

WI-7830d	150	C/T	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCCAAATCTTTTCCCCTTCTGTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCTTTGATCCATAACTTTAGT[C/T]TAATGTACACATTGCTGCACTTTTTACTTTTTGCGTGTGTGGA
WI-7830c	54	G/A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGAAGTCT[G/A]TCGTCTGATGATGGATAGGGGGCCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACGATCCATAACTTTAGTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGTGGA
WI-7830b	134	G/A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/A]ATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGTGGA
WI-7830	44	A/G	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCCAAATCTTTTCCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGTGGA
WI-7865e	25	A/G	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C/T	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]CGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C/T	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C/T	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]CGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

ID	Position	Allele		Sequence
WI-7865	25	C	T	CCACTTCCTATCTGATTTTTCCCAGC[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGGAGAGATGAATCATTCTACCTACTACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAAATCACCATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAA
WI-7865	191	C	T	CCACTTCCTATCTGATTTTTCCCAGCCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTACTACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAACCTGAAATCACCATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAA
WI-7867c	92	A	C	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTTCACCCTTCAGCCTTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGCCTGTTGAGTTAATGTTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGTCTATATGTCTATTTAATTGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A	C	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTTCACCCTTCAGCCTTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGCCTGTTGAGTTAATGTTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGTCTATATGTCTATTTAATTGATGCTTAAGG
WI-7868c	173	C	T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAACAAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCGGGCCAGATCTTCCACGTCTCCACGTCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCTATTCAAGCAA[C/T]TTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C	T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAACAAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCGGGCCAGATCTTCCACGTCTCCACGTCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCTATTCAAGCAA[C/T]TTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T	C	TTGATCGATCTTTTCCCACCCTGTCCCTCAACGTGGTCCCTAGAACAAGAGGCTTAAAACCGGGCTTT/C]TCACCCAACCTGCTCCCTGATCCTCCATCAGGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCTATTCAAGCAACAACTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85	T	C	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCC[T/C]ATTTATCAGAATCTCTGTAATTGAATATAAATGTTTACTCAGAGGAGCTGCAAATTGCCTGCAAAAATGAAATCCAATGAAATATTTAAAACATCATTACTGCCATCTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

ID	No.	Alleles	Sequence
WI-7870	76	C T	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTTATCCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAATTGCCTGCAAAAATGAAATCCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54	C	TTTATCATGAAGCACATCAATTACAAGCTGTGAGACCTAATATCAATTTG TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACCAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCCAAGGCTGTCTTCTCCCAGAGCACGAAG
WI-7889b	54	C	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACCAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCCAAGGCTGTCTTCTCCCAGAGCACGAAG
WI-7894c	142	A G	AGCCCACCCCCAAATATAACTGTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTTGTACT TTTACTATATCTACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]TATGTAAAATTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCATA
WI-7894b	142	A G	AGCCCACCCCCAAATATAACTGTATCCAGAAGCTGTGTATGTCCTGTTTCCATACATGTTTTTGTACT TTTACTATATCTACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]TATGTAAAATTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCATA
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC

		C	T		
WI-7900d	128	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATTGATCATGAATAGGAGCCCATGCCTGAAAACTCAACTATAGAAGACATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900c	84	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900b	128	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900	84	C	T	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCCTGCCATTGAAACAGTGATTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7901c	33	C	T	---	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACACAGGACACATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTCGTGCGGGTTATTGGGGCAGGCCGCGGTCGT CACTCAGTCGCTCTCGTGTCATACAGACACAGGTAACCTAGTTCT
WI-7901b	33	C	T	---	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACACAGGACACATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTCGTGCGGGTTATTGGGGCAGGCCGCGGTCGT CACTCAGTCGCTCTCGTGTCATACAGACACAGGTAACCTAGTTCT

ID	Pos.	Allele 1	Allele 2	Sequence
WI-7901	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACATATTAAACAGATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTATTGGGGCAGCGCCGGTCGTCACTCAGTCGCCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271	T	G	AGACTTAGGTACAATTGCTCCCCTTTTTATATCATCTGCATCTATTTCCATATAGTCATCAAGAGCACACACAGGACCATTTTATAAAACATGGTAAGACCCTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTATTGGGGCAGCGCCGTGGTCGTCACTCAGTCGCCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C	A	CATTCCGCCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATTTACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTAGAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28	A	T	CATTCCGCCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATTATTTACAATGCAATACTTACATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTAGAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150	C	A	CATTCCGCCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATTTACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTAGAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203	G	T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCACAAGGCCAGGTCCTGTGCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCCTGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCGAAGCCACAGA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7947	203	G	T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCACAAGGCCAGGTCCTGTGCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCCTGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCGAAGCCACAGA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7963b	145	T	C	CATGTGCTGCATGAAGAGCTAATTTAAAAAAGCAAAGTAAGTAAGCTAATTATTTAAAATAAAAATGCCACAAATTTCATTTCTCCTTCTAAGTATTACAATGGAGTTTATTCTCTGCCTAAAAAGTGGAAGAAATTGAGTGAATGA[T/C]AATTTGTAATTTAGGATAAGATCCAAGTTATTTCCCCAACTCTGTGTTTCCCCCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAAGGCAGAAGACGGAAAA

WI-7972c	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCTGTCACCATTCCTGTTCCAGGAGGGCAGCATGCGGGCTTCCTGTGTGGGGGAGG GTAGAGCGGGAGAAAGGAAGGGCAGCCAACCAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGGGAC...
WI-7972b	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCTGTCACCATTCCTGTTCCAGGAGGGCAGCATGCGGGCTTCCTGTGTGGGGGAGG GTAGAGCGGGAGAAAGGAAGGGCAGCCAACCAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGGGAC...
WI-7972	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCTGTCACCATTCCTGTTCCAGGAGGGCAGCATGCGGGCTTCCTGTGTGGGGGAGG GTAGAGCGGGAGAAAGGAAGGGCAGCCAACCAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGGGAC... AACCCCTGAAATCGGAAGGGACTTCCTCTCTTCTCTCCCTGTTTAAATTATAAGATGTCAT CCCCTTGTGTCAGAGACAGACCCCTTGGCTTTGCTGGCAGAGGAGACCCCACTGGACTGGGGTTTTG TCTCTGCATCTCATTGGTGGCTGGAGCTTGGTCTGAGCTTATTAAGATAAATAGAGTTCCAAATA
WI-7981	261	T	G	AGGATTTGTTCACATGCCATCATAACCATTCCCATTGGTTCCTCCTAAAACAT GAGCTTCCACAGTGCAAGATGGAGAAGGTGAACTTGCTTTGAATATNCCAGATTGTTGGTC[A/G]T GCGTATGGCAGTGGAGCGAGCAGGTATGTGTTTCTTTCTTCACGAAAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTTGCTTGC
WI-7992b	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTTGCTTTGAATATNCCAGATTGTTGGTC[A/G]T GCGTATGGCAGTGGAGCGAGCAGGTATGTGTTTCTTTCTTCACGAAAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTTGCTTGC
WI-7992	62	A	G	ACTAAGAGAAATTATTATTGGTGGCCTATAAAACTCTGTTCAGTCTTTACCTTGCTAATGATTTATTT CATTAAAGTAAATGATCATCTTTGGGGAGGCATTTTATAAAAACATATTTAGGAGAAAATTCTTTGA TTTATGCTATAAAGGTAAATGTTGCATAATTTCTTGCCTATGTGAATTG[C/T]AGGTTTCCACTTTGAG AGAATTCTCTCAATCTAATAATAAAGACCAAGGGCCAGAAACACTAAGATA
WI-8004b	183	C	T	ACAAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCCACTTGCTTTGGTACTTGTGTGAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTGCGGCCTCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8021c	57	C	T	ACTGGTCCTTCACTTGCGGCCTCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCCTTGTTAGGGGTGATTCGGTGAATTGCCA

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WI-8021b	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCCACGTCTTAGAAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGAACTGGTCCTTCACTTGCGGCCTGTTGTAGGGGTGATTCGGTGAATTCGGTGATTTTACGTTGCGGCCTGTTGTAGGGGTGATTCGGTGAATTGCCA
WI-8021	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCCACGTCTTAGAAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGAACTGGTCCTTCACTTGAGATTCTTTCTTTGCGCCCTCTATCAAGTCGGTGAATTGCCAGATTTTACGTTGCGGCCTGTTGTAGGGGTGATTCGGTGAATTGCCA
WI-8024c	206	A	G	CTGAAAATTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCAGCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGTGGGCCCCAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTCAGCCGCCTCTAGCCTCTAATTCCC[A/G]CTCTAGAAACAGCTGGCCTGGTCGTCGATACACAAGGAAAGAGC
WI-8024b	206	A	G	CTGAAAATTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCAGCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGTGGGCCCCAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTCAGCCGCCTCTAGCCTCTAATTCCC[A/G]CTCTAGAAACAGCTGGCCTGGTCGTCGATACACAAGGAAAGAGC
WI-8077	167	A	G	GAATGAGCCTTCCTAGCCGCCGAGGGACCTGCTGTGTTGGCCTGCACATGCATTCTATGGAATGCTTTTTGGGCCAAGCGGGGGGCCACTGAGGACTAAGCTCTGANNNNNNNNNATCTCGCCCAAACTCCTTCTAAGGAGTCTGGGGTGTCATGCCCTACAAACC[A/G]TAAATTCTCATCAGATGGATTTTATTTAACGTTGTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAACAAGGGAAAAA
WI-8118f	114	G	C	TCTAGGGTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTT[G/C]TTTCTTAGCCTTGAAGATGACCAGGTAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	G	TCTAGGGTTAATCAAAGCAATTTGCANTTTGGA[A/G]TGACCACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTCTTAGCCTTGAAGATGACCAGGTAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	TCTAGGGTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGTT[T/G]CTTAGCCTTGAAGATGACCAGGTAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

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WI-8118c	44	C	T	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGA[C/T]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATTGGCTGTTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	T	C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACTAGCTGTTTTCTTAGCCTTGAAGAAGCTAT GTACTTCATGCTGTGGAAAC[T/C]GGCAAATACAGAATGTAGCTGTTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA AAAAATCAGGACTGTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	C	T	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGAAGAAGCAGGAGACCCTCTTGGCACACA TTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAAGAGCACAATGAAGAGAGCACAATGAAAACAATCACGGCA
WI-8171c	46	A	G	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGAAGGCAGGTGGGAGGAGGTTCCCTGTTACTTAAGAGAA ACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGGATGATGATAAAAACAATCAC GGCACCAGTGGGCAAAGAGCACAATGAAGAGAGCACAATGAAAACAATCAC
WI-8171a	46	A	G	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGAAGGCAGGTGGGAGGAGGTTCCCTGTTACTTAAGAGAA ACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGGATGATGATAAAAACAATCAC GGCACCAGTGGGCAAAGAGCACAATGAAGAGAGCACAATGAAAACAATCAC
WI-8171b	298	T	C	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGAAGGCAGGTGGGAGGAGGTTCCCTGTTACTTAAGAGAAGGC TTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGGATGATGATAAAAACAATCACGGCA ACCAGTGGGCAAAGAGCACAATGAAGAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85	G	C	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGCCCATTGCAATTTCTTGGGTCTGT TTCTCTATCT[G/C]AGGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78	C	G	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGCCCATTGCAATTTCTTGGGTCTGT TTCTCTATCT[C/G]TAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

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WI-8321	178	G	A	TTTTTAAAATATGCCCGTTAGAGCAGAGACACAGTCACAATAAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCCACTTTCAGTATGGTTCAGAAT(G/A)AGTATCTTAGTATTCTTTCTA TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT(G/A)AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTATTAGCTGAACTGTTGGC
WI-8321	178	G	A	TTTTTAAAATATGCCCGTTAGAGCAGAGACACAGTCACAATAAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT(G/A)AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTATTAGCTGAACTGTTGGC
WI-8332b	123	A	C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA[A/C]ACTAAGTAG CAGTACTGTTTGGTGTGTGTTGTTTCTTCCCCAGCAATGCCTACTGCACTTAGTAACAACTAG AGGTGGAGGGNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A	C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTCCCTGTGC[A/C]GCCTTAGAAACTAAGTAG CAGTACTGTTTGGTGTGTGTTGTTTCTTCCCCAGCAATGCCTACTGCACTTAGTAACAACTAG AGGTGGAGGGNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T	C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAGAAGAGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGAGANTTCCAATCCAATCACCTNTCACCNTCCTCCAACACGTGGGG AACTGCCCCCATGATCCAATCACCTNTCACCNTCCTCCAACACGTGGGG
WI-8378	308	T	C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAGAAGAGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGAGANTTCCATCGGGAGACACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCNTCCTCCAACACGTGGGG
WI-8426	184	T	G	TTTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAACAG TTGTTGTAGACTGTTAANNNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTCTTTGCTGTGGANGGGNCCCGGGGCCCTTGAGCTGTGGTG AGGCTGGGGATGGGANGGGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCAAGTTTAGTTTCAATCATATTATACCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGAGGATGGGAGTGTAATATGAGCAGTACAGATTCTTAATGCAATTCAT

ID	Pos	Nuc	Sequence
WI-8450g	55	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAATTCAT AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450f	108	T A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAATTCAT AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450e	125	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAATTCAT AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450d	125	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450c	108	T A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450b	61	C A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTTCTCCAAGTTTTAGTTTTCAATCCCAATTATCCCCTCCACTACCCAGCAAACTAC AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGCAATTCAT
WI-8450a	55	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60	A G	CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTATTTTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTCGTCACACACTACAAACCTTCAC ACCTGGCTACAGCAATTGTGACTTACATCACCATTGTTATACTTGTGAAAACTTATTGTGCACAGT GACATCCATTCCGCCCAGACTTAATGTTATAAAGCAGCTAGAGCAGAGTTCTCA

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WI-8461c	105	A	T	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTAGACAAAGAGANTAAATGATATAATATAAATCATTTTT[A/T]NNNNNNNNNCCTTGTCTTATTCACATTCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAAGTTATTACTTAAAACATCTGTGTGACCTACATCAAAGAAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T	C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAATTTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTNNNNNNNNNNCCTTGTCTTATTCACATTCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAAGTTATTACTTAAAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T	C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAATTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTNNNNNNNNNNCCTTGTCTTATTCACATTCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAAGTTATTACTTAAAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A	T	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGAGATGACTTAATTTTGATAAAAAATTAAAAAGCAT[A/G]AACATGCATATAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTCTGCTCAGTAATTAAATATTCTTCCCTTGTTTTTGTCTTTTAAAAAACATTATTCTGAAAAAAAAAATCAGAAAAACATGATCGTGGAGAGAATTATTA
WI-9438	77	A	G	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTAACTTTTGATACAAAGTAACATTTTAGTACAGAAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGCACTGTACCATCTCAGTCCCACTCTGCCTGTAACTTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTACAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439b	101	C	T	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTAACTTTTGATACAAAGTAACATTTTAGTACAGAAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGCACTGTACCATCTCAGTCCCACTCTGCCTGTAACTTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTACAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439a	76	C	T	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTAACTTTTGATACAAAGTAACATTTTAGTACAGAAAT[C/T]CCAGTCTGTCAGCTCAGTACCTGTGTGCACTGTACCATCTCAGTCCCACTCTGCCTGTAACTTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTACAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9446b	75	T	C	GAAGGCTTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTATAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAACCTTTAAATTACTCATCTTTCATATGTGTTGTNCCCCTACTNTTATCACTGTGTCTTCTGTCTTTGTCTACCTATGNAACTGCACACTATCTGTGGCAATATTGT

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WI-9446	75	T	C	GAAGGCTTGATTAAGGGAGGNTTTATTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTAAAT TACTCATCTTCATATGTGTTTGTNCCCCTACTNTTATCACTGTGTCTTCTGTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A		ATTAAAATGTCAAGGTTCATGTGTTTCATTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTTAGAGTGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A		ATTAAAATGTCAAGGTTCATGTGTTTCATTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTTAGAGTGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG GTGAAAAAGTTTCTATTCATTCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTATCTAAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTCCACACATTGTA[C/A]AGTG AAAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523b	193	C	A	GTGAAAAAGTTTCTATTCATTCCATCATACAATAGATTGTGCTAAG[G/A]ATCATTTTGGAAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTATCTAAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G	A	AAAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATACTGCCTTTNCTAGTTGTTATTGTACAAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAGAACAACACTAGAGTCCTACACCCAAGTACAACATATGATAAAGCAGCCCTCGCAAGTG GT[T/C]GCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTACTGCTTATGATTTT
WI-9554	202	T	C	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAAGGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9555	97	G	A	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGAAAAACTTTGGAAAAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAAAACACACTGACAAATCTTTC
WI-9625b	172	A	T	

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WI-9625	172	A T	TTGAACATTTAATGAATGACAAAGAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAACTTTGGAAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTA[T/A/T]GTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTAAAAAAACACACTGACAAATCTTTC
WI-9647	144	C T	TTTTTCTGAGATTCAAAGAGCTACATTTTTGGTAGTGTATGTCTACTATACCTTTTTCATCCTTCA ACATCTTTTGTCACATTTAGGTGATGCTATCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACT[C/T]GTCCTTTACCTGATACATTTATTCCATTTACTTTACTTGGATTTTTAAAAATGTTA ACTTAATACGTCTCTTTCAGATGTCCCTGCTTTTTAGTTAATTGTGTT
WI-9676n	114	A G	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676m	184	G T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676l	84	A C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C[T]CAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676k	202	C T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAG[C/T]CAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676j	92	C T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676i	173	T C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCT[T/C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT

ID			Sequence
WI-9676h	134	C A	GGGCCACTGTCTGTCACAGTCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676g	202	C T	GGGCCACTGTCTGTCACAGTCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676f	184	G T	GGGCCACTGTCTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCCAACCCACATGGCTT[T/C]CCCTCTGTGCCGCATGAAATAACTTGA GGCCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676e	173	T C	GGGCCACTGTCTGTCCAAAGTCTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCCTATGCCTATG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676d	134	C A	GGGCCACTGTCTGTCCAAAGTCTGTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGAC[A/G]GATGTGGCTTTCCTGCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCCTATGCCTATG GGCCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676c	114	A G	GGGCCACTGTCTGTCCAAAGTCTGTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCCTTCCCTCTGTGCCGCATGAAATAACTTGA GGCCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676b	92	C T	GGGCCACTGTCTGTCCAAAGTCTGTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGAGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCCTTCCCTCTGTGCCGCATGAAATAACTTGA GGCCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676a	84	A C	GGGCCACTGTCTGTCCAAAGTCTGTGTCACAGTCTCCTCCATATGGCAAGAAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTCTTTTATAAATGCAGAGCAAGAGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCCTTCCCTCTGTGCCGCATGAAATAACTTGA GGCCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT

WI-9738b	40	C	A	---	TGGACCAAACACAGACAGAGTGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTT GAGTCAACAAAAGACTCTGCTTGTCACCTGCCTGGACGCGGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTTCTGTCCCTTATTGTTGGGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C	A	---	TGGACCAAACACAGACAGAGTGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTT GAGTCAACAAAAGACTCTGCTTGTCACCTGCCTGGAGCGGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTTCTGTCCCTTATTGTTGGGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A	---	---	ACTGAAATGTAAATGGCCAAGGCACCCAGGACCTTAAAAATCATAAGAAGTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAGAGCAGGAGGATGTGATGTAATGTGTCCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACAGAATATACACTTTTGGAAG ATTTCCACTTAACCACTTGATTCTTCACTTTTTATGATTAAAACTCTCCGTGG
WI-9758	135	A	G	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGGAGAATTCAATTCAAAGAAGAGAATTCTTGTTCGCAAGGTCAATTTTATACTATTTA A[A/G]TAAAATAAACTCTGGTAGGTTCTATAGCAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAATT ATTACG
WI-9778	127	G	A	---	ATTTAAATCCAGGCAGCGGGGAAAATGGATACTTTCATATGTCTCTGTACCCAACTATAAACTTTG GTTCTCATGCACCATTTCATTTGCCTTCTCCAGTACCACTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAAATGTGTCAGTCGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C	A	---	TCTCCCCTTTGCCTCCTCCATGCCCACTCCCCTGCCACAGAGCGGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTC[C/A]TGGATCCCACCCAGGA CTCAAAAAACTAGGAATTGGGAGAGAGGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101	A	G	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGTCTGATAAAAATATAC[A/G]TGTGTATGTAGTATATATTAACACTT TATGAAATTCCATTTTGAATGAATAAAACGTCTGTAAGGATAAACTAAGGTTCTATCAGTCGGGAAATGAGA AGGATTATATACACACAACAATAAAAACGTCTGTAAGGATAAACTAAGGTTCTATCAGTCGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGACTATGCTGTTG
WI-9880c	222	G	A	---	GAACTAACACCTTCTTCGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCGTCTGTGTGGGGTTGAGTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAGATCCTCTTTAAAATTATATTTATATAAGCACATGAA AATGGAATGAAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C	A	GAACTAACACCTTTCTTGCATGGATTTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGA[C/A]TATATTAAGATCCTCTCTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACACATATTTG
WI-9880a	108	C	T	GAACTAACACCTTTCTTGCATGGATTTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATTAAGATCCTCTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACACATATTTG
WI-10183	127	C	T	ACACTGCAGGCACTCCAAATCCTNACAGACACATATGCACTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTAAAAAACAACGCCCCAGTTATCACAGTTTCTNTTTTGTC[C/T]CACC ATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGAGANACTCTCTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC CGGAC
FB25G10	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC CGGAC
IB3071	102	C	A	ACAAGCGCTGAACTTCCATAACAGTCAATGGTACAGTCAAACATCACATGTACAGAACACACAATTTA GATGAACTGAAATTATAAGNTAATAAAATAAAAT[C/A]CAATTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTCCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTGTAGTGA GGCATTCACAAATTGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C	T	CGTCCTTTCCTTTTGAGATTGCAATTAAGTAGTAGATAATATGAGAGGAGAACTGACAATTGGGGTGTCCC TACTGAGCTTGGGGCCCAGGTGTGTACTTAGGAACCAATCCCACCCAGAAGAGACTCATCTATGTA ACACTAAGGATGCCCTCGGAGGAGGTC[C/T]TGACCACATACGCGGCCATTGGTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51	G	T	AGCATAGAAAGTGATTTATATTTTTAATGGTTTCAAGTGGAAGTTCCTTT[G/T]AATTTGTCAGTTC ATTCCTGGAAAATCTTTGAGTTAAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAACCACACAGTGCTAACTTCCTCCCCTTTCGTCCATTGGTGTTTTCAGTGTCTGTA TTGCAAAGTCCTGATGCTGCTAAACAGTATTTGGGAGTGTTTTCAGTGTCTGTA

ID	No.	C	T	Sequence
UTR-00481	115	C	T	TATTCTTTTATCCTGGGGCCACAGTTCTTGATTATTCCTCTGTGGTTAAAGACTGAATTTGTAAACC CATTCAGAGATAAATGGCAGTACTTAGGACACAACAAACACACACAGA[C/T]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTGTAGCATTTCAGATTGAGC
ESTC1	33			CCCTGTAGCAGTCTTCAGCCTCCTCTACCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37			GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21			GCCATCAAAATTTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20			TGCTGGCTCACTTCCTCACANGCTGTATACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35			AAAACCAGGAAGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23			AAACCTCACACAGAAAAGAGGANAACACTCAGAAAATGTGATTACAGATTAGGCA
ESTC113	37			AAGGGACACAGTGTTGCTGACAAGGTGACACTGAACANAACAGTTTCCTTAATTGTAAAGCGGG CATCG
ESTC117	24			AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAGC CTCCA
ESTC119	24			TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34			GACAATAAACAGCTAAGCTACTGACATAAAATTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21			GAAGCCAGTATGTTGTGGCAANATTCGAGAAAACACACTGAAAAA
ESTC128	42			GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAA TGTGGAACTGG
ESTC129	20			AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46			GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49			GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	CCAGTTTGGCTTCTGTCCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	AGGAGCACAGCCTAAGGACACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGGCTGGGTCCCTGAGCTAGGAGGAGG
ESTC14	20	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGCTTGCCCTGGTG
ESTC142	72	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTTATTCATTTAAATCAAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCTTTTG
ESTC144	26	AAATCCATATTTCTTGACATGAGGTNGCTTTTAGCAGCATTTCGG
ESTC146	20	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	TCTTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCCTGTGGAGGCCCCTGGGGGTGGCTGGGCCTGTGTCCTGAG
ESTC149	28	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	GGATTGTAATATTGCCAGCTTTGTGAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATATATCAATATTAAACCTGATGTTTAAAGAAACCTAATGAGA
ESTC151	49	GAAGCTAAGGCCCCATTTTTTTTCTTTAATACAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGAAACACAGCC
ESTC155	37	TTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATTATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCTGGCTGCGCTCGGGGATGGAGCGGGGCGGCCTCACCACCACTGCAT
ESTC158	35	ACCAAGCCCTGGGATTTACTGTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGCAA
ESTC159	31	AGCTGGCAAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTAGGGCACGGTCTGGTTCTGCAGCTTTGAAAGG

ESTC16	23	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGCACAGTGATCATCCCCACAAGGACAGGTT
ESTC160	38	TTCTAGCATTGCTGGTGCTGCAGTGGGGGCCTGAGCTGGGGNGCAGTCGCGCAGTGTCACTGGCGCCCGTTTGGGACTGGGTTGA
ESTC162	36	CTCTTCGTCCGTTTGCAAGTTGCTGTTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	TCATTCTCCATAGAATATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAAACAATCCGATACATACCA
ESTC169	22	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCGCCGTCTGTTTCCATGACTT
ESTC176	23	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	TGGGTGGCTCTTTAAAATACCTTCCATTATATTTTCAAATTTNCTTTATTCTATTAAAATACCTTTATTCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	TCAGACACTGCCGACACTCAGCATTGTCTCNTGTACAGCTCCCTTCCCGCAGGGCGCCCCTGGGAGACAACTGGACAAGA
ESTC181	21	TAGGGATTCCAAGTTGCCTGGNTTAATATAATACATATTCACAAAATTTACACAGCTCATGCATACCA
ESTC186	43	GCTTGACTAGCGGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTGATTTTCACCTCA
ESTC187	24	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	TCTATTAACAGGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCACTTGTCTTCCATCTTGC
ESTC189	27	AAAGTACAAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	TCCTCAAATACCACTTTCCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTACCTTTCAGGGG
ESTC197	26	ATCTCCAGTGTGTCTGCGTCCTCCCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	AAGATTAGGACAGACCGCGGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAACGCTGCTTAGATC
ESTC200	44	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAAAAAATCATTANCATCATTAACAGTACTTAAATCAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	TCTTACTTGGGTAGTTTAGCAAACATTTTTAAAANCCACATCCAACAGATTGGTT
ESTC202	22	CTGCTGGAGGGAGGACAGACGGNCAGGCGGCCCTGGGTGGCGCCCAGAAAGGCTGGCGTGGGATGTT CGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAATATCCAAATNAAATTACTGCAACTTTTGTAGAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAGC CTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGGTAACCTGATGAGGAAGCTCTAGTGNGAGAAATTCAGGAGGTCTTCAGAGCAGGAGGGCTTGGT TCAAGTC
ESTC214	21	CTCCAGAGTCCCTCCTCCTCANACCAGGGGCAGGAGGGAGTTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTTACACTAACAAATTAATTAATCACAGTATTNTTAGATTGGTCAGAAAAA CAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAAATAACATTAACAAGTTCAT AAACACACCCA
ESTC219	32	GTACACATCCTGGGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAAATTATGGGGTTTATTCTTATTTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGGGCAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAAACACACACACACACACA TGCCACTGTTACTCCCCAGACNGAGAGCTTACATACCCATATAGAAAGAGCATAAGTGCTTCAGAAGGA
ESTC225	20	ATGTGTAGGGATCG
ESTC23	27	TTCTACTTTATTTCATATTCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAATTAAGA
ESTC231	24	CAAAAGGGGTTAGTCATATTCCCCANCAACAGCATGATAAAAATAATTCAAC

ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTTCTTCCTCTATTCCTCTATAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	CAGACATGACCTACCGTCCCNGGCCCTCAATTCATATTTTATTCTTGAGCCGCCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAAACAATATATTNTCAGTCGGTGATCATTGTAATATACAATACAAAG CAATTTCCTCAGA
ESTC33	25	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTAAAAATATTTGACTTGTTCCCCCTTCAC
ESTC45	37	TTTGGAGGTTTGTGTCTGGAGTTTGTTCTTTGTAACNCTCTCATCATCGAGGCTATATATTAA
ESTC50	56	CTGTCCGTGGTGGTGAGCCCTGCCGCGTGTCCCATGGGCCCAGGAGCCACTGGTGCGGANCCGGGCCAGATG TTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAAGGACCACCA AGT
ESTC57	20	AAGTGGGCCCTCCCAGTCCCNTCTCTGGGCACAGATCCCACCAGTCTGCTC
ESTC59	38	GAAACACAAAAGTGTTGAGAAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATG TGGACTGAACCG
ESTC61	57	AGTGATTTTGGCTAGGCGTGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCAANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACACCANAGGGCCCACGGGGAGGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGGANACCCTCAAGTTTAAATCCCACACTTACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	AGTTCCCTAGAGCTGTGCGGCCAGATAGCGTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACT G

ID	No.	Var.	Sequence
ESTC72	37		GGGCTTCCAAAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCTAAAAAGTGTGACC AACAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCATCACNTTGGGTTGAAAAGTTG GAAGA
ESTC74	49		... ...
ESTC77	40		ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20		GGCTCAGCACAGGGATAAGANCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25		TTTCAGATGATGGGGTCTGAGATGTNTCCTCAGGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53		CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28		TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC89	22		ATTGCAAAGGAAGTGGAAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33		CTGGTTCTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCAGTGCTCCACCCAAGTGTCCTTCCGGATGAT
ESTC93	29		CTCCCCTCCTCAGTTCACAGTGGAGACTANGGAGGATTCAGGGCAGGATCC
ESTC95	32		GCACGTTCTTGTTCTCTCCTCTTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
DWU-100	127	C T	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCCTTGACTGTTCTCCA(C/T)GCCAG ATTCTTATCAATGATCTTTCACCTAAGAACAGCAAAGATTCTGGCAAGCACGATCTAGAGATAC ATCTTATTGGCGATTTTCACAAAAATCAAAAGAAGAAGAAGGCTTAGCTG
DWU-177	77	A G	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAGACGCCTTGTGCTGAA TGTTCATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAAACAACCCAAGCTATATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATGATCCCTACTACACTGTGGAT
DWU-286	213	A C	CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAAATTCCAGCGGTGCCACCCAATCATGCCCAGCTTCTGTCATATGAATGAGATATACATTT ATGTCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

DWU-252	94	A	G	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCTCA[A/G]TGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGAATTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C	T	---	GAACATTCCTCTGCAGCACTTCACTCACCAAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTCTAAAGCTCGAACAAAAGCTTTCTTTCCTTTTGCAA CAAGACAAAGCAAAGCCACATTTTGCATTAGACAGATGACGGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A	G	---	GAAAATGTTAATTGGGCAGGTGAAAAGGTACAGATGTCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCATCATTTCCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGGCCTGGCTGGCTGGAAAAAGGTGAATGTTGAGGGCCCTTCACTCCATCCAACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCT[A/G]GCATCTATTCCTCTGTGC
DWU-1537b	89	A	G	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAAGGGATTCAGTTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C	T	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAAGGGATTCAGTTGTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGAGCT ACAGCATTTTCCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C	G	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGAGCCCCTGGGAATTCCAGGTCCACTGTTCCTTCCTCGTCTCCTGTGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG[C/G]AGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCCTC
ESTD-ADAa	184	G	A	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGTCCAGGTCCTGGGAAT CAAGCCCAGCTCCAGGCCCAGAAGTGGGACATGGAGGCCCTG[G/A]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCCTC
ESTD-ANT1	160	T	C	---	TCTCGTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A	G	---	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTCTTATCTCACTTGATGATGTTCACATTGGGGCTTGGGGCTTCCAACACGGAGAAG CATTGTTTTCTTCCGGGCCAAGAGGTATCTACC[A/G]TATAGTGTCTATTAGGCATTTG

Name	Pos	Allele		Sequence
EST10398 2a	147	C	T	TGCCTGGGGTGGCAAGGCTGCAAACAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTAAGATGCTGCCACCTCTTACTTGATGATGTTCACCATTTGGGGCTTCCAACACGGAGAAGCATTG[T/T][C/T]
ESTD-C7	14	G	C	ATATCGTGGCCTTA[G/C]TACCTAGAGCTGGACAATCCTGCTGGA
ESTD-D4S95	90	T	C	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTGAGAAGGAGCAAAACAACTTTCAAGGATAATGGGGCAATCACTTTCTTTT[T/C]TCTTCTTTAGAGTCTACCGG
ESTD-GPPK2L	38	G	A	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACC[G/A]CCGAGAACTGCTCGATATC
ESTD-HRASb	82	A	G	CTGGGCTCGCCCCGCAGCAGCTGCTGGCACCTGGACGGCGCGGCGCCCAGGCTCCACCTCTATAGTGGGGTCGTATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD-HRASa	37	C	T	CTGGGCTCGCCGCCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GCGGCGGCCCAGGCTCACCTCTATAGTGGGGTCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-NRAMP	81	A	G	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCCAGGTCCCACAGACCCAGAGAAGCGGCCTCAGTGTATCCCCACCCCA[A/G]TGTGGGCGCTGGGAGATGAAGGAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A	G	GTGACCTTCTCACTTAA[A/G]AAACTTACCGGAGGAGAAGAAATTAAATATATGCTATGGCTATCAGCAGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
EST36751 7	36	C	T	CCAAGTCGTTCAATTTGCAGGTTTAACT[C/T]GATTACTTTTTCTATTCAAATCTCTGTAAAATTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTAAACAG
EST40562	109	A	G	CACGTGGAAAGGAGCTATTTTGGAGGCTTAAGAGTAAAGAATCTGTCCCCAAACTTGTGGCTGACTTTATGGCTAAGAAGTTTCACTGAGTCATTAATAACAAAT[A/G]TTTACCTTTTGAAAAAATAAATGAAGGATTTGACCTGCTTGCGTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACAGATGCCTTCCCCTTGTAGCAGTTTCAGCCTCCTCTCTACCCTA
EST18288 3	121	C	T	GCTCTCTATACCCGTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAAGATTGACAGGTTCATGCAGGTTGTGACAGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGTGTGGACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTGCTGGCTCTGGCCCCTAGGGACTTTAGTATCC
ESTD-AK-168	31	C	T	GGGAGTGACAGCTAGAGCACCAAGGGGGCGGGGCTC[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTCATTCTGG
ESTD-ALB	180	A	G	AATCCCAGCACTTTAGGAGGCTGAGGCAGGCAGATCACCAGGCAGCATATCACCAGGAGTTTGAGACCAGTCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGTAATCCCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGAGATCGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC

			Sequence
EST70523 3	182	G/T ---	TTCCCGGCCAGCCCCATCCTTGGCACCCTGGTCCCCCTCAGGGGGCCACCCCGGCCACTCACCGCTCT CGCTCTCGGTAACATCCGGCCGGGGCCGCGTCCTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGCTGTCCCGGCCCTTGCCAGGGGCCAGCCCT[G/T]CAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD-APOA2	101	C/T ---	CCAGGTGTTGTGGCACGTGCCTGCTCCTGTAATCCCAGCTACTCGGGAGGACTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGAGATCG[C/T]GCCACTGCACTCCAGCCTGGGTGACAGAGC AAGACTCC
EST58707 7	112	C/T ---	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCACATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAAATGGACAATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137	C ---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGCGCAGGCGTGTCCAAGGAGCTGCAGGCGCCCGGCGCGCGGGACCATGGGAGGA CGTGCGCGCGCCCGGTGCTGCGAGTACCGGCGCCCTGCCCAAGCTGCCGGTAAGGGGCTCCTC TGCGGGTGCCGCTCGCCCTCCCACCTGCCCAAGCTGCGGTAAGCTGCGGTAAGGGGCTCCTC
EST43211 8	132	C ---	CGCCTGGTGCCAGTACCGGCGGCGAGGTGCAGGCCATGCTCCGCGCAGAGCACCGAGGAGCTGCGGGGTGCG CCTCGCCTCCCACCTGCCGCAAGCTGCGTAAGCCGGCCTCTCGCGATGCCGGCGCTGCGAGAAGCGCC TGGCAGTGTACCAGGCGCCGGGCGGCGGCCGCCGGGCGCGCCGCCTCAGCGCGCCATCCCGCGGAGCGCGGCTG GGGCCCCTGGGTGGAACAGGGCCGCGCCGCGCCGTGCGGGCGCGCCGCCCACTGTGGGCCTC
ESTD-ARSB	126	A ---	GGAAGAAAATGGAGCCTGTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAGGGGCGTGAAGAACCGGGAGCTCATCCCACATCTCGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C ---	TGTAGCCAAAGTCACCTGCTCATCATCATTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCTGGGCCTGACCAAAAATATACTGGGTTTCCTGTTTCCTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAAGGCTTATG
EST26021 1	137	A/G ---	TAATGTAAGCTCATCCACCAAGAAAGCCTGCACCATGTGTTTGAGGTTGAGTGACACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACCAAATGA GCATTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTCTTTTGCAACAAGACAAAGCAAAGCC
ESTD-BA511	29	A/G ---	GGGCAACATAGTGAAACCCCATCTCTACA[A/G]AAAATACAAAAATTAGCCAGGTGGTGGTAGCAAG TGCCTGTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGATCCCTTAAGCCTGGGAGGTGGGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA

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ESTD-BCL2	116	A	G	---	AGCTGGGATTATAAACTCTCTCTTCTTCTCTGGGGGCCCGTGGGGTGGGGCTGGGGCGAGAGAGGTGCCGTTGGCCCCCGGTTGCTTTTCCTCTGGGAAGGATGGCGCACGCTGGGAGACAA[A/G]GGGTACGACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTGCAGAGGGCTACGAGTGGGGATGCGGGGAGATGTGGGCGCCCGCGCCCGCCCGCGGGCCGCGCCGGGCATCTTCTCCTCCA
ESTD-BCR	69	C	T	---	CAGTGGCTGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGAGA[C/T]CAAAGAGGTCAGCTTCTGTTCCCGGGAAAGGGAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAAATCAACCATCCGGTGGACACTGTGTGGCCGCCATCTGCCATCTGCCTGGCACA
ESTD-BRCA1aa	119	C	T	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAAGTGGAGAAAGGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]TTGGTACCTGGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATAAAT
ESTD-BRCA1bb	139	A	G	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAGAAACTTTGAGGAACATTCAATGTCAATGTAGTGTCACCTGAAAAGAGAAATGGGAAATGAGAAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTTTTTAAAG[A/G]AGCCAGCTCAAGCAATATATTAATGAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA
ESTD-BRCA1cc	126	A	G	---	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA[A/G]AGGAGAGCTTAGCAGGAGTCCTAGCCCTTCACCCATACACATTTGGCTCAGGGTTACCGAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122	A	C	---	ATCCTGAGCTCGCCCAATAAGCTTCTTGGTTCTACTTCTCTTCTCCACAAGCCCCAATTTCACTTTCTCAGAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA[A/C]AAAGGCCCCTCTCTACATCT
ESTD-C1R	40	A	G	---	ACACAGGTGCTGGCCACTGGGGGCTGGGGATCCTCCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C1R	40	A	G	---	ACACAGGTGCTGGCCACTGGGGGCTGGGGATCCTCCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	31	A	C	---	CCCAGTCAGTTTGGGGGACAGCCATGCACTG[A/C]GCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAAGCTCTCTGCAAAAT
EST201182	119	C		---	GTTCCGGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGTGGTCCAGCTGAGGTGAGGGGCCTTGAAGCTGGGGAGTGGGGTTTAGGGACCACGGGTCTCTGCGTGCATCCTAAGCTGCTGTGCGTGCATCCTGCGTGCATCCTAAGCTCTGAGA
EST530186	67	A	G	---	ACAATCCAGGTCACACATTCCAGAAGAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC[A/G]GGGATTCAGGAAGAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

Name	Pos			Sequence
ESTD-CB22	119	C	T	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAGGCAGTGCCTAACTGGGGATGGACAGACAATCAAAGAGCCAGTGCCAACCCATAGGG[C/T]GGATACAAAAGACAGGCAAGGAAGGAGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGCTTCATTATGGTCCTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	136	C		TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGCTTCATTATGGTCCTTCTCTCTCACACATCACTTCCCTTCCCACACAGAGGAGAGCCCTACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCCTTCCCGAGAGGATCTCCACCACCCAAAAGGTCGCTGGTGTGTTGAGCCATCAGAAGCAGAG/AGATCTCCCAACCCAAAA
ESTD-CB24	145	A		ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGAGGTCGCTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAGGCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACACGACCCGCAGCCCTGAGCGTGGGTGGGTGAATGGGAAGGAGGTGCACAGTGGGTCAGCACAGACAGACCCGCAGCCCTCAAGGAG
ESTD-CB25	146	A	G	GTTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTCTATCTTTCGCCGTCTCTGCTCTCGAACCAGGGCATGGAGAATCCACGGAGCACAGGGGCCGTGAGGGAGGCCAGAGCCACCTGTGCACAGGTA/G[C]CTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGGTCCTGTCTGCCACCATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	125	C	T	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAATTGTGTGTTGGGCCTGGTTGCATTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGAC[C/T]TATCTTCTGATTAGGGAAAGCAGCATTCCCTTGGACATCTGAAGTGACACCATTCCATACCGCTTTCTCCGTGTTCATCCTGATGGAAGTCCTCAAACACCATTCCATACC
ESTD-D4S338	59	A	T	TTTTCTGTTTCACCTTGTTCCAGATCCCTTCCAGAGGAATCCCTATATATGGCAGGTATATGA[A/T]ATGTATTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAAATGTTATTTAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATTGCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCAATGCAGTAG
ESTD-CYP2D6	61	A	G	CAGGCCAGGCGTGGTGGCTCGAGGTGGTCACCATCCCGAGAGAACAGGTCAGCGAGCACCACCACTATGC[A/G]CAGGTTCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTCTGCAGAGGCCGAGAGCATACTCGG
ESTD-D11S1873	40	A	C	AAAAAAACATTTTAACACCTTTCAATCATCATATACACCCATA[A/C]ATTTCCATTTTCACATAAGTCAGTTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCAATGTCATAACTAACTGATCATAGCTGACACATCCAAGCATCTACGATCCAGATCTAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCACACAACTTTCCCAAGCACATCCAGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGGGGTGTATCTGCATGTC
ESTD-D17S33b	169	C	T	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCCTCTGACAGATACACTCAGGGCCGTCATGCTGCACACATCCAGGGGCGCCCTACCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGGGGGTGGGGTTGTGTGGCTATGTGGTCTTGTGTAGA[C/T]GGGGGCTTGGTTCAGTTGCACTATTGCGTTATTGCAGATTGCTTTGTCTTTGTCTTTCCACCTGAGCGAGCCTC

Marker	Position	Allele		Sequence
ESTD-D17S33a	75	C	T	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTG[C/T]ACACATCCAGGGGGCGGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG GTGGGGGTTGTGTGGCTATGTGTGGTCTTGTGTAGACGGGGCGCTTTGGTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	133	A	G	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCC[A /G]GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACCACTGCACTCCAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD-D3S11	44	G		AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAATCCAATAAAGTACACTGTAATAAAGAATTAACAGAATATCATTGT TTATTCAAACTATTATTCACTTATTTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	37	A	G	AGGTTCCACATTATTGCTGATGTTCCTGATGTTCC[A/G]GGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTCAAAAACTCTCTACAGCCGTTGTTGTTATTAATTCAAGGT TGAACATAAAGTA
ESTD-D3S2b	247	C	T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCCTTTATTTGGAAGGATGCC[C/T]GGT
ESTD-D3S2a	248	G		GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D7S399	83	A	G	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTCAGCCACCTCCATAGAT AACTGCTAGAGACCC[A/G]GTCTCCTACATCCTTTCACAAACATTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146	A	C	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCCTGCACGTGTGCCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGAGGAGGAGGAGTGGGGAGGGGAGACA GAATGCTGATT[A/C]TCTGGTGGAGAACCAGAACTTCTGCCGGCCCTGTGGGTAGGGGCCAGCTGCTTCCAAG ACCTCCTGATTTGAGGGAAGGGGGCAGCAGAGCGCGAAGAGAACAGAGT
ESTD-DMa	66	C	G	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCCTTGCACGTGTGCCTCAAGCTGCTCGGCCCTCCA[C/ G]TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGAGGAGGAGGGGAGGGGAGGGGAGA CAGAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGCCGGCCCTGTGGGTAGGGGCCAGCTGCTTCCAAGA CCTCCTGATTTGAGGGAAGGGGGCAGCAGAGCGCGAAGAGAACAGAGT

ESTD-DRD1	154	C T	TCCCCAGCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTGCCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGAATTGCTCTGGGG[C/T]TCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	144	C	TCTGCCTTTGGTGCAGGAGGCTGCCCGGCGGAGCCCAGGAGGAGATGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCCCGGTACAGCCACCCCATCCCACCCGACCCCGCCAAACCAGAGCTCTCCCCGACCCG TCCCACCACGGTCTCCACAGCACTCCCGACACTCCCGACAGCCCGCCAAACCAGAGAAGAATGGGCATGGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	109	C T	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGTAGGAGAGGGCCATGTGGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGTGTAGTTCAGGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGTGAGGAGA
ESTD-ERBB2	93	C T	TCTTTCAGGATCGCGCATCTGCGCCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCCTCCACCAGCTGG GGTGAGGGGTGGTGGGTCAGTGC[C/T]GGGGGCCGGTGCAGCCCCAGCGCGGGGCTGGGAGGACTTCA CCCCGCCTCACCTCCGTTCCTGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	43	A G	ACTCACAGTGCTTTAAGTGAAAATGGTCGAGAAAAGAGGCACC[A/G]GGAAGCCGTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACA CACAGACTACTATTTTTAGATTTTCTTTTGCCCTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAG AGGGTAGGAGGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGAGTTAGTTTG
ESTD-F9	111	A G	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCCATTTGAGTTAATATTTGTGTAAAGTAATGATGTTTA[A/G]GTCAAACTTCATTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAC
EST687875	144	A	CTTCCTATGGGATTTGACTTATTTCTCCATTGTCTTCTTTACAGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTGAAGCTGACAATTACACAGAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTCGAAACATTGAAGTTGTTTTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
ESTD-GCDH	200	C G	CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGGAGGAAGGAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCGTGTGCTTGCAGAGAAGAGGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGCGCACCGTGTTCTGCTGCGCCCTGTTCAGCTGTCGTCGCCGAGTC[C/ G]GACTCTGTCCCGGAAATTCCGAGAGCT
ESTD-GCK	88	A G	GTTTTATGCATGGCAGCTCTAATGACACAGGATGGTCACAGGATGTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAGAATCCCCACCACCCCCACACCTGGC TGGAGCAGGAAATGCCAGCGGCCGCCTCCCCAGGGAACGCAGGCCTAGGAGTGTGAGAGACACAGTC ACCTGCCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG

ID	Pos	Allele	Sequence
EST34088 2	62	A/T	GTGGGGGCAACAGTGGGAGAGAAGGGGGCCAGGGTATAAAAGGGGCCCAAGAGAGACCGGCTC[A/T] AGGATCCCAAGGCCCAACCTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD-GNAT2	56	A/G	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[A/G]GGCCATCA TTGAAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
			GGGCTAAAATTTCCGAGCAACTTTGCATAGACTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGGAGGAAGATGTGTTACAGTTGTCAGAGAGAATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACCTT
ESTD-HT2	154	G	AACACACAAGCCCCAGCGAGAATTGAACTCGCGACCCCTGGTTACAAGACCAGTGCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTTCTTCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAAATTCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTCGAAAGGTTCT
ESTD-HT5	149	C	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTTCTCTTCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCTGAACCAGCAAAGAGAAAAGAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTCGCGTCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST37382 5	124	A/G	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCCAGGAGGTGC[C/T]CTGGGAGAAGAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD-IGFBP1	43	C/T	TTTTACTATTTCAATGGATACAGAATTGTGGGGAGTCACTATATTCCTATGAACAAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAAGTGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IGHV4-6	120	C	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTACTATTCATTATTATTATTATTTTATTTTTTG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAG[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTCATGCGAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCGCC ACTGTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1A	110	A/G	CCACTTACAGATGGGATAAATGGGTACAATGAAAGGGCCAATAGCCCTCCCGTTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGGCTGTTCTTCTGCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
ESTD-IL1B	99	A/G	TCCAGGGTGGCTGGACCCCAGGGCCCCAAGGCAGCAGGGACGTGGCTGGGCTCGTGAAGCATG TGGGGGGTGAGCCCAGGGCCCCAAGGGCCCTTCAGCCTCCCGAGTGCGCCTGTGGATGCTGGGCC T[CCCAGATCACTGTCTCCTCTGCCCCAGCGCCGCAGCC
EST74082	134	A/T	CTCTGGGGACCTGACCCGAGCCCAGCCAGCCTTTGTGAACCAACACCTGTGCG

ID				Sequence
EST45311 0	151	C	T	GCCCTCCTCTTCCAATTCTGTCCTCTATTAAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGGAAGGATCCCATTATTGTGGCCATTGTAACA CATTTTCTGCAAAT[C/T]ACCTCTTCATTTAACAGCCCTTATTCAATGCCCTTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80	A	G	TGCCCCATCACGGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC[A/G]CCCTCAAAATGACAGCCATGGCCGGCCGGGTGCTTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGCACAGTCTTGCATGGACACATCAGTCAGTCTGATTAAA GAGGTTAGGTGCGTGTTTCCTGTCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26	A	T	ATGCAGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACTGTCATCCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
				ATACTAGTACAAGTGGTAATTTGTACATTACACTAAATTATTAGCATTGTTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTACCTTAAATGCTTATTTAAAATGACAGTGGAAG TTTTTTTTTCCTC[G/T]AAGTGCCAGTATTCCCAGAGTTTGGTTTTGAACTAGCAATGCCTGTGAA AAAGAAACTGAATACCTAAGATTTCTGTCTTGGGGTTTTGGTCATGCA
EST62782	149	G	T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTGCT[C/T]TGCTTTTTAAATAGT CTCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT10b	183	C	T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTA[A/ G]GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTTAAATAGTC TCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT10a	133	A	G	ACCCTCACCCCTCCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGGTCTTAAGAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCCAGGTTTACCA[C/T]GTCAACATTGACACA
ESTD-KRT8b	231	C	T	ACCCTCACCCCTCCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGGGTCTTAAGAGACTAAAGAGAGGGCCAGAATGTTACAAAAGTGAGGCCCATA GGCTGCCTATCTCTCCCGTCTCCAGGTTTACCAGTCAACATTGACACA
ESTD-KRT8a	21	C	T	
EST75099 6	82	C	T	CACTTGTGTGTCTAGATCTCCTCAGTGGCCGCCCTCTACTGGCCACCGGAAGACCATCTTGGAGGATGAAAGAGGGGCTGGCCCACC AGCATCGATGTCAA[C/T]GGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGGGCTGGCCCACC CCTTCTCCTTGGCCGCGTCTTTGAGGTGTGG

Name	Pos			Sequence
ESTD-LF79	142	A	G	GGGTGATTTTGAGGCTCAGTTAATATTTCAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCCTCTGCCATGCAGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGGCTTCCCTTACCACCCAGA
EST358799	142	A	C	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTCCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCCTGGAAGACAGCAGCGGGGGATGGGGCGCAGGAGGAGAGCTGCCTGGATGA A
ESTD-LMP2	35	C	G	TACACACTTTCCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113	C	T	TGTCAGTGTCCCCTAGGGGCACCTCCACCACTTCTTCAGCTCTGGCCTGTCCTGCTGCCTGCA AGGGTTTTGCTTAATTCTCAATTCAATGTCTCTTCATCTTTTAG[C/T]AGCTGTGGGGTTTTGTTGTTG TTCTTCTGTTTTTGCTTAGTATCTGACTACTTTTAATTATAAAAGAGATGTATCTTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATTAAAATTTTTCACCTG
ESTD-MCC	45	C	T	TTGTCAGGAGTGTGTGCTGATGCTGCCTCCCCAGCTCGTGTCCCTAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD-METH	118	C	T	CATCCATGTAGGAGAGCCTTAGTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAGGGTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTTCTGACG ATCTTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	25	A	G	ATTATCCAGATGAATTTACAAAACT[A/G]TACCAGATCCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107	A	G	AACAGGACTTGTATATTTGTACAAAAAAAAGTTTATTTTTCTAAAAAGAGAAAAAGAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACCTGCCTA[A/G]GCCCAAAACGTCTTATTGTGGT AGGATCAGCCCCTCATTTGTTGCTTTTTGTAGGGGACGAGAAAGATCATTGAAAATCT GAGAAAACTTCTTTTAAACCTCACCTTTGTGTCCCCTGGCTGTTATCTTC[A/G]GTACTGCAAAGAGAACACA
ESTD-NPPA	45	A	G	TGTCCCTAGGCCCCAGCCCCTGCCCTCCCTGCCCTGTTATCTTCTTTTCTGCAGGCATATAGAATTTGGT GACAT
ESTD-NRAS	202	C	T	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGTGATTATATTAGCAATTTGAGGG GGGTTTCTTTATGTAGGGTGATATTGGATACTTTTGTTGTGATTATATATTAACCTTGGCAATAGCATTG[C/T]ATTCCCTGTGTTTTTAATAAAAT
ESTD-PAI1	100	A	G	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTTGACACAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGG[A/G]GTCAGCCGTGTATCATCGGAGGCGGCGGGG CACCATGGCAGCAGGGGGATGAGGGGAAAGACCAAGAGTCCTCTGTTGGGCCCAGTCCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT

				Sequence
ESTD-PAR	120	A	-	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAATTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTCACTTTCTGTGTTCTAGAACGTTTCTAG GACTGGCAGTTAAGCTTCACTTAGCTTCACTTAGCCTTTCACTTAGCCTTTCTGTATACCCATGCCC
ESTD-Per/RDS	74	A	G	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCGGAATCTGAGAGAGGAGAGCAGGGCTGGCTG CTGGGAGA[A/G]GAGCGGTGCCGGAGACCTGGAAGGCCT
EST68308 5	29	C	T	GGAAAGAGATTTAAGAAGCTTGATTTGGA[C/T]AATTCTGGTTCTTTGAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	39	A	G	GGAATATTTAAAAATATTTTAAAATACCTCCATTTGCTT[A/G]TCCTTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	ATGAAACATGGTTCTTTAATTTATGTATGATATGTTTGTTATAGCTATCTTAAAAGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAAA[A/G]GAGCGAGCTGTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
				CCCGGAATCTGAGAGCGAGAGCCGTGCTGGAGAAGAGCGTGCCGGAGACCTGCGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACCAGGTGCAAGGCGGCAGCAGG CCCAGGCCCCAGAGCCCGGAGGGCCCTGGGCCCCTCCCGAACCTCGCGAAAGTCTGAA CCAAGAAACGTGGATCTCCCCCTCCCCCTCATCCAACTCGAAAGTCTGAA
ESTD-RDS	127	A	-	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTC[G/T]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
ESTD-s14544	94	G	T	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCCTGGGAGAGATGG[A/C]TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST52908 0	45	A	C	AGGAGAAGCTGAGGAGGGGAAGGAAGAGAGAGACAAGAATGACATTGATGAGTGAAGATGT[C/T]GGCTCAG GATGCCGGAAAATGAC
EST19590	55	C	T	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACC[C/T]GCGTCATACCTTTATCTATAGCCTT CCCCTAGGTCTT
EST76136	39	C	T	
ESTD-SPTB	176	C	T	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCCTGGGAGCCTGAGGAGTTGTTGTGTCTGTGTG CAGTCCCCGGCCGGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCGGAGAAGAC ATTTACCCACCTGGCCATGCCCTGGTCCTGGCCGTTGTTGTGCACA[C/T]CCTCTGTGTGGAAGACCCCTGC CTCCCCCACCCACCAAGCCCAGTTTCCTAGCAAGGGCAGGAC

Label	Pos	Variants	Sequence
ESTD-TAT	224	C	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTGTGTGGGACAGGATCA ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTCTCTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	125	A C	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGTTGATTCCAAGAGAAAGAGTCCCAAG CACACGAAAAACAGAAGTTGCAGATCCCAGTCTCAAATCACACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TYR	122	G T	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGCAGCTTCTGTTCCCACCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAAAGCTGGTGCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGGTGTTGATCCATTTTCATTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYRP1	222	A C	AGTAGTGGATGAAGCTAACCAGCCTCCTCCACTGATCAGTATCAATGCTATGCTGAAGAAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTCTTCTTCACTTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A C	AGTAGTGGATGAAGCTAACCAGCCTCCTCCACTGATCAGTATCAATGCTATGCTGAAGAAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTCTTCTTCACTTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-VB12	148	C T	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12b	148	C T	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGT·ACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12a	74	A G	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATGTCCAGACGTCCAAGAACACAAGGTCACAGAGAACAGGAACACCA GTGACTCTGAGATGTCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

Name	Pos			Sequence
EST58607 0	105	A	G	CTCTGGATGGGTTCACAGGTTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAGGACAGCAGCCACA[A/G]TGGCGCGGGATGGCCGGCGGGAGTTC TGGTTGCGGCCACGGCTGTGGCCTGCGGGGTGCCATCGCCTGAGATGTAGATGCGGCC TTCTTGGCCAAGGAGGGGCGGGGTGT
ESTD-VWF	36	G		AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189	C	G	AGCACCACCTCTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTTGGTGGTGGA AGGAGTGCCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGGCCATCCAAGG
ESTD-TNFAb	152	A	G	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCCATGAAGGACGGGGTTCAGCCTCCAGGGTCCTCACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTC[A/G]GAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGTCCCAACTTTCCAAATCCCCGCGCCCGGATGG
ESTD-TNFAa	88	A		TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCCATGAAGGACGGGGTTCAGCCTCCAGGGTCCTCACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTTCCAAATCCCCGCGCCCCGGATGG
EST52418 6	113	A	G	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGAGTTACGGGCGCTCAGGCGCATACACTT[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89	A	G	CCCACTCTATTTGCCCAGCCCCAGGGACACAGAGCTGATCCTTGAACTCTTGAACTTCCACATTGCCAGGA CCAGTGAGCAGCAAACAGGGCC[A/G]GGGCTGGCTTCATCAGCCTCCCAGACCCTGGCTGCAGA CATAAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCCTGCTGCCTGCCC CCGGTCACTC
EST51976 7	123	A	T	AGGCAGAAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCAGGACAAG[A/T]CTCTCTC CCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGTCAGAGATGCTG GCCCCTTTGGAGAGCTGAGCTGCCCCTGGTGC
EST11458 6	140	A	G	CCACTTTGGTAGTGCCAGTGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTGTTCTCGAGTTT CTCTGCCCATGTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCC[A/G]TTAAAAACATTCTATGAGCCAGGAAAGAGATTACGTATTCCTGCCAAGCGGGCTATGTG TCCCGAGGAGGGGATGAGAAAGTTTATCTGCCCTCTCCACAGGACTGTGGCC

Name	Position	Allele 1	Allele 2		Sequence
ESTD-AT3aa	60	C	T	...	AGACCTCAGTTTCCTCTCTGTGTAAAAGGGAGAAGTTTGTTCTTGGATCTCCATGGGCCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCGTGTATCAGGTAGAGACAGATATTAAGAGCTGGGAGAAGTGG TTGGAATTCAGACAAGAACAAAGAGACAGATAT
EST398528	106	C	G	...	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTA[C/G]GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST624480	112	A	G	...	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCCTCTTGGCATTGCGGCGCCCTGGGGCCCGTGG TCCTCCTGGTGCTGGTGCTGTGGGGTAGTCCTGGAGTCAACGGTGTCCTA[A/G]GTGAAGCTGGTGTGATGGCA ACCCTGGGAACGATGGTGTCCCCAGGTGCGCGATGGTCAACCCGGACCAAGGGAGGCGCGGTTACCC TGGCAATAT
EST360272	120	A	C	...	AGTGACTTCCAAGGAGGAAATGGCTACCCAACTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATTCTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTGAGATGGCTGCTCTCTAAAAAGACAAATGAATGGGGAAAGACAA
ESTD-COL2A1cc	112	A	G	...	AGAAATGTATATAGTCCTCAAACTGGCCATCTCCATTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCCTGTCCACTTTC[A/G]GGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCGCTGTCCGCTCCCAGGTAAGTCAAGCATATACAAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1dd	97	C	T	...	TGAGAGAACACCTAGTCCTCCTCCATCCTCTCTCCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGGACCTGGAACA[C/T]TTGGACTTCTTTCTACTGCAGCACAAGAGACTTA CCCAAGAGAGAGATTAATGGCAAAGATATACAAATACAATTTTATTGACCAAACACTACTCATGGAACA GCATT
ESTD-CPT2	150	A	G	...	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGACATGTTGATGCCTTAGAA GGCAAATCCATCATCAAAAGTTAACTTCTGGGCCAGATGAAAAGCTACCATCCACTTCCTCATCATGAAAAC TGGGAGGCCGGGCAT[A/G]GTGCTCATGCCTGTAATCCCAGCATTTGAGAGGCTGAGGCGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST122740	135	A	G	...	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCCTCCTCATGCCAAATATTCTTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCCACCATGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACCACAGAGCTTGCCAGATC
EST76807	91	G		...	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCATC CAGCTGCCACTCACTCAATGGCCCAGCCAGTCAGCCCAGCGGCCCCAGCGACTCACCACTGCCCCCT GCTGCCCATGTGGACTGGTGGTGCAAGTTGAGGACTTCTTG

ID	Pos			Sequence
ESTD-SSA1	111	C	T	TTCACTTTGTGGATTGTTCTTTTGTGTGTGCAGCACCTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTGGCTGCCTGCCTGTGCTTGCTGGGGATATTGAAAGAGAT[C/T]TTTGCCAGTGCCAATGTCCTAGA GAGTTTCCCAAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTAATCCATT TTGJATTTGATTTCTGTA
ESTD-RYR1	109	A	G	CTTCGTGACGGGGAGGTCACGTCCTCCGCGCCTCCCGCCCTTTCATGGACATATGGATGAGTGTGACCATTTCCC CTGCTGACAGTGATGATGACCAGCGCAGACTTGTCTACTATGAG[A/G]GGGGAGCTGTGTGCACTCATGCC CGCTCCCCTCTGGAGCCTGGAGCCACCCTGCGCTGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTCACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70	A	G	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTCTTACTCTCTGCCTGCAGGATGTG CG[A/G]CGTGTCTGCGTGGAGTAGCCCCGACTCTTGTACGGGTCGGCATCTTGAGACCAGTGAGAAACGCCC CTTCATGTGTGCTTACCCAGGCTGCAA GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCCGTAGGGGAACTGGGGGATCCAGGGGTAGGGGTGAGGAATGGCCC AGCCCAGTCCCCGGCCGGTGCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGGATGGGGC TGGGATGAG
ESTD-F2 EST444387	100 62	C C	T	GCAGCCAGGAGAGCCGCTGCACCATGCCCCCGCATAGATGCCGAGCCTCAAGCTCGGACTTCAAGGA[C/T]G TCCTGCTCGGACCTAAGCGGAGCAGCCTCAAGAGCCGGAGGTGGG
ESTD-PBDA	103	A	G	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTCCGTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGGCTGGGAGAGGGCAGGAGCATCCCAA[A/G]TCTCTACCCGCAGCTTGCTCGCATACAG ACGGACAGTGTGGTGGCCAACATTGAAAGCCTCGTACC
EST128393	122	A	G	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGTGGAGAGCAGAAATATGGTCTCTCTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-CTLA-4	48	A	G	ATGGCTTGCCTTGGATTTCAGCGGCCACAAGGCTCAGCTGAACCTGAACCTG[A/G]CCAGGACCTGGCCCTG CACTCTCCTGTGTTTTTCTTCTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-ACE	96	C	T	GATCAAGCAGTGCACACGGGTCACGATGACCAGCTCTCCACAGTGCACCATAGAGATGGCCATATA CAGTACTACCTGCACGTACAAGGATCTGCC[C/T]GTCTCCCGTGCGTCGGGGGCCAACCCGGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTGCTCGGTCTCCACTCCTGAACATCTGCACAAAATCGGCCCTGC
EST544198	88	A	G	CTTCTGCCTAATTTGAAATGATATTGTTGCTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTA TTTCTTGACCCCTACTTAC[A/G]ATCCTGGAGATGTATTTGGGTTTCCTGGGGAGATGTATTTTAGCGTTGTTGGTTGTTGTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99	A	G	GGGGAGTAAAACTTGGATTGGGGAGAGATTTCATTTTCTACAGTGTTCTGGTTGGTGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAACCATAGCCT[A/G]TTTCGTAGCCATATTAATTGGTTGTGCCTTAC ATTATTACTCCTTGCCACAGATTATCTTGTA TTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104	C	T	GGCTGCCAGGGGGTTCCGTGGGAGGCGGCCCTAGCCGGGGCCCTGGCGCGCTGGCGGGTGCTGGCCACC GTGGGAGGCAGCCAACCTGCTGGTCATCGTGGCCATCGCC[C/T]GGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTTGACTTCGCTCGGCCGCGACCTGGTGGTGCCGCCGGCGGCCCA CCTTGGCGGC
WI-567b	48	A	G	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCCTGGTTC[A/G]AGCCCTCATCTCTCTTTA CAGGGATCCGCCCACAGCATCCCAACTGATCTGGCCTTAGGTCTTCTTCTCCAATCCATTCTTCAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATTCTGATGCTACCATCTTGCTCAAGCC
WI-801c	58	G	T	ATGGAACACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCTT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCAATGCATGTTTGCAGGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-801b	58	G	T	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCTT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCAATGCATGTTTGCAGGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-1099b	76	A	G	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATTATTCTGAAATATTAT TTTTACA[A/G]TACCCTTTGATTATTTTGATTCATTTGTAACGAGAGATTACAACATATCAGTAACGC TGTTCATTGATAGTGCTATCACAAATGTCTAAAATACTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71	C	T	AGGAAATGGCTGATACTCCTGGTGGCTTCATTATAGTAGTAAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/T]TCTTAACTGCTGCTGTGAATAAGCTTGAAATAAAGTCTACACAATTAATTAGTGT AAGTTGTAAATGCTGAAATAAAGTCTGAAATAAAGTAGGTAAAGAAGAGGAGAACTGTGCTTT TTAAGAAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205	C	G	TAAGGGCCCTGTCTTCCCCCAGAGGCCCCACGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGACCTGTACCCTATGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGGTGGCCAATTAAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTTAACATTTTAGAC AGG[C/G]AGCAGAAGCAGCAAAGGAGGAGAAAGGAAGT

Marker	ID	Allele 1	Allele 2	Flank A	Flank B	Sequence
WI-2625	98	G	A	---	...	GGGCAGTCCTGGCTGTGAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAGAAACAGGCAGAAGCACTGTGGTAGTAACAAGGCTTATTAGGA[G/A]CAAATTGATGATACTCCCTGAGGACTCGCAGAAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCCACTTGCAGGAGGAAAGCCAGCCAGCAAAG
WI-2924	54	G	A	TGACCTTCCTAGTCTTCTCTTATAGG	GCCCTAAGTGTAATCACACAGGG	TCTGTTGTCATATTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTCTTATAGG[G/A]ACCCTGTGATTACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72	G	T	GGCTTGTCTCAGTGCCTTT	CTTGTTGAGGGAAGGTCTTG	CCATTGTTGAGGTTGGGTGGGGTCACTTGTCATTCCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGCC[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTTCCATGCTCCCGTGTTCTTTGAAAATTCGACTTTATCCTGAAAAACTCAGCTGTATAAAGCCACTCCTG
WI-3203	99	G	A	GGTTATGCCGCAGACGAG	TCAAGTATTGCCTTGTGTGG	CTTGCTACCATGCATTTCACAGCATACAACCCTCAGTGAAATGCCGTAAACCCCATTATAAACATCTTGCCATCGAAGGGGTTATGCCGCCAGAG[G/A]CAACACACAAGGCAATACTTGAAGTGACTTGGAGAATAAAGATTTTGGATGGATGAAAGCAGAAGAGGAGATGCTAAAAGTGA
WI-3473	101	A	G	AAGCATTTAGCCCTAGGGA	CCTGATGTCACCAACATTTCT	GGAAAAAGAAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTAGTTGGTGATAGGCCCTGTTGGAGATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[A/G]TAGAAAATGTTGGTGGTGCACATCAGGGCT
WI-1796b	29	A	G	...		ACACACTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTCTGCACATGGTGATATTTAAGCAGGAGAGCATTGTCTTGGCTCCCC
WI-1796	29	A	G	...		ACACACTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTCTGCACATGGTGATATTTAAGCAGGAGAGCATTGTCTTGGCTCCCC
WI-4360	93	C	T	GTAGTCACATTAGGTATTTTCCAAATAA	GAGAGATATTTTCAGAGGCATTTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGTAGTCACATTAGGTATTTTCCAAATAA[C/T]AAAATGCCTCTGAAAAATATCTCTCCCATGTCCCATGTCTAAATATAACATTTCCC
WI-1959b	87	C	T	...		GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAACAGGAACCAAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1973b	28	A	G	...		GTTGTGCCTGTAGCAGACACAGAGGCCA[A/G]GAGGAAAAAAGCCTTTTGGTCCAGGGGCCTTACACTGAATCCCTCAAACAATGCAAGATGAGCTAATGTGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACAAAGGTATAGGGTTTG
WI-1980b	140	C	T	...		CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAAGCTGGAACTAATCCCCCATATACCAAGGGACAAAATTGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAATTTTTAA[C/T]GACAGTTTTAATTGAGTGAAATTACCTAAAATAATAATAGTAGCAGCTAATATTTACTGAGCTGTTACTAGGTGCCTATAAATAGC

Label				Sequence
WI-2015b	190	A	G	TGTCAGATAGTCCGTCTCTACCTAGGTGCTGCAGTAGCATGCTAGGAGCTATTAAAAGTACACAATTATGCTATATATTATACAATATACAATTACTTGCAGATAGCATGCTAGTGAACCCCACAAGACTATGTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGCTTTTCCAACT[A/G]CATATACTTCTAATACCATAGAG
WI-754b	49	C	T	GAAGGCACAGGGAGGAAGATGGCTGTCATCTACCAGCCAGGGAGAGAAGC[C/T]ACATTTATTGGTAATCCTATAAAGTGCATTCTTTAAAATTTGTATTTACTTTAGA
WI-754	22	T	C	GAAGGCACAGGGAGGAAGATGGC[T/C]GTCATCTACCAGCCAGGGAGAGAAGCCACATTTATTGGTAATCCTATAAAGTGCATTCTTTAAAATTTGTATTTACTTTAGA
WIR-1b	56	A	G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTGGAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-1	56	A	G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTGGAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-3b	72	A	G	TAATTTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAAGAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A	T	TAATTTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAAGA[A/T]GTATCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-4	47	T		GAGCCTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCAAGGCAGCAGCAAATTTGCCCAGCTGCC
WIR-5g	209	C		CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5f	196	C		CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5e	194	C		CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG

Marker	Pos			Sequence
WIR-5d	191	A	---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCACTGTTGGTCGGCTCTCATGGAAACACAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTCATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177	C	---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCACTGTTGGTCGGCTCTCATGGAAACACAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTCATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159	A	---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCACTGTTGGTCGGCTCTCATGGAAACAC AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTCATGGAAACAC AGGTTTTACGTCCAG
WIR-5a	37	A	G	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTC[A/G]CAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTCTATGGAAACAC AGGTTTTACGTCCAG
WIR-6	63	A	C	TAACCCTGAAACTTGTCTTCCTCATCTCAGGGAGGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTTCTTGGGGTTGGGGCAG
WIR-7	12	C	T	TTCGTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46	C	T	GGGGTCCTATGACTATCCTGGTCATTGATTTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56	C	G	AAACAGAAAAATAGAGGTTATAGGATGGAACTAAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAAACCATGGCTTGATTACT GACAAC
WI-7069	93	G	A	TGTCCTTGCTTATGCCTGCCTCTTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAGAGAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAA TAAGAGATCCTTAGTGCACCCAGTGACTGACATCTTAACACAGCCGTGTTCAAAT GTACAGTGGTCCTTTTCAGAGTTGGACTCTAGACTCACCTGTTCTCACTC
WI-18694	41	A	T	GGTCATTTCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTATTACCAATAATACAGTTCCTTATATGAGGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37	A	G	...TTGTATTGCTG CTTGCAAAT / CCTATATTTCA AGTTTGGAAA TGC	CACACTGTTCACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT

ID	Pos	Allele 1	Allele 2	Flanking seq (a)	Flanking seq (b)	Sequence
WI-18517	87	C	T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAAATCAACTAGGGCTCACCCTCAACACCCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]TGTTGCACTTGTCCAAACACAACTGACTGC
WI-18668	76	C	T	GGCGAAAAAC TAGGCAAAAA	GCTAAAATTAAA CTGCACTTTTT GC	GCTAAAATTAAACGATTGACAAACCTTTATTTTCAACTTAGGTAACAGTCCAAAATCAGTGTAGATTGGCGAAAACT AGGCAAAAA[C/T]AGCAAAAAGTGCAGTTTAATTTAGCAAAGGCTCAAGACACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T	C	GCTGTCACTCT AGCATCTGGA A	CCTCCTGAATA TACAACGGAGC	TAAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTGTCACTCTAGC ATCTGGAA[T/C]CGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTTCTCCGA GGGGTAC	CTGG	CACCCAGGCTGTACCCAGGCTTCTTGTGCGAGCACCACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[A/C]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---		TGTGGGCAAACCTTGTTTAATTGCAAAC[A/G]ACTTAATTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GTCGTGGGGTG GGGG A	GCAAATACCAC TGAAGAGGAC	GCAAATACCAC ACCAGTCATGTTTTATTGGAGGTTAATTCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCCTCACGGAGGGGCTCGGGGCCCAAGGTCGTGGGGTGGGGGGGTCGCAGA[T/C]GTGTCCTCTTC AGTGGTATTGCGGACC
WI-18533b	91	T	C	---		GGGGAGGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAAACTCCCGAGATTTCTTCTTTATTT TATATTTCATTTTCATCCTAA[T/C]TCTTACTGAAGCCATTTTTCTTGGTTAACTTTAGA
WI-18533a	59	T	G	---		GGGGAGGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAAACTCCCGAGATTTCTTCTTTAACTTTAGA TTTTATATTTCATTTTCATCCTAATTCTTACTGAAGCCATTTTTCTTGGTTAACTTTAGA
D11734	83	A	C	TCATCTGATAC CTTGTTCAGAT TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTCAGATTTC[A/C]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTT
D49493	159	A	T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGCTGCAGACACAGAGCACAGTCCATGGCAACATCACTGGGCCCAGAGAG AGCTGTCCGCCCAGTGCATCATTAGGGGGTCTTTCATTGCTGGCCCTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCTGGCCTGAAAGTGGCCCATCATTCATACCCCACTGTT CT
EST100307	98	T	C	CATTTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAATTTT CCCTTAGCCATTTTGTTCTCTCTCAAGTCCCT[T/C]TCATCCATACCACCACTGCTGATTG
EST100052	24	G	A	GCTCACTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCATCATAACCTGGTGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118	C	G	---	CTTGCGTAAATCACAGTTCTGTATTCATACAAAAACTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61	T	G	CTCTCAAGTAG ATAAGAGGCA TAATCT / GCTAAATTTC AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAAATTCTTTCTGAAAATTTAGCTTATGAACTCATTACACTGCAAACCAGAGAAGGAGCAC
EST11260 8	101	G	T	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAA
EST11349 9	109	C	T	---	TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCCACCAGTAGAATTCTTTGGACGAAGAAAATCCT TCTGTGGATTCAGCTTTACCGCCCTTTCCTCATCTGCTGGTGT[C/T]TTCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI-16632a	71	A	G	CCAACCTACTT TGGAGCCCT / TCCAGCTTTCT CTAAAAACTCC T	GAATTCTGGGTATTAAATAGCGGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTGGAG CCCT[A/G]AGGAGTTTTTAGAGAAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGGAGTGGGAA
EST11772 6	74	A	G	---	CCAGGAATAAAAGAAAAGAAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAATACATTCAGGAGCTCA
EST11795 3	82	G	A	---	CTTGTCCATTTATTTGTGCATGTTGTTCTTAAAAGGCTTGTGTGAAAGATAACTTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42	G	A	CAATAAGCAG CTCATTTTGAT TAC / ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAATTC ATGAAGTAAAATTCATTATACCAAAAAGCCTCCCACAGAACTTTCATGCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56	A	G	TTGTATAATA ACACTCAGTA CAAAGTCTGT / GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCATTCCATAGTTTTGAAATC
EST12055 9	32	T	C	---	GTGGAAAATTTTTTTATCTGTACGTCTTCC[T/C]ATTATATTATCTTGTCCTTGATTCAGCACCC CACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAGTCTTCT
EST12492 1b	95	A	G	---	CCCCTAGCAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCCACAGCAAAATTGACGATGCAGCTTTTTA CCTTTTTA
EST12492 4	25	A	G	---	ATCTTGAGGTTTCTGGGCCTGTCAG[A/G]AAGTGACATCTTTACTTACCACAGGTCAGGAACCCTAT AAAGAAACTGTGTAGAAAGATATCAGGTCAGACTTTTAAAGGGGCTTCTTATCAGCTCAATAAA

EST						Sequence
EST12502 2	52	C	G	---		ATAACTAGGGAGGAGAAAACCAAACTGGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGAAATGACCATTTTAAGGGCCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105	T	C	---		CCAGAGAAAAATTAGAATGTATCGGTAAAAGAAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCCTGAGA[T/C]GATGCATGTGGCAGACGAG
EST12620 0	67	A	G	---		TTTTCTTCTCCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22	C	A	---		TTGGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCCAGGTCATTGCG
EST12941 8	23	T	A	---		TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAGTTATTCACCAGAATTTTGTTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTGTTTG
EST12949 2a	52	A	G	GGCTTAATCA TAACCTAATA ATACTGTT	TGTGTCCTGT GGGTCTC	AGGGATTTCATGAGCTTAATCATATAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTTCCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104	C	T	---		ATTTTTGTTTCTTAAATGAAGCAGTATAATAAACAGTTAAAAATTCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAGCAGCTTCCCACCCAAG CACCTCTGAACT
EST13117 6	66	A	G	---		TGCTGTCTGCATCAGTCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTACTGTGC TTTACTG
EST13121 6	44	C	T	---		TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTCCTGTGTGCCAGGCCAGTCTCCTCCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74	T	G	---		AACTGTTTACTAACAAAGGTGCTTAATTTGAAAAGCATTGGAGGAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACCAGTTCTACAAATTTCACATATCCGTCACTGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72	G	A	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTACTGAACTTACAACCAACTTGCCGCTCAATATGCCAGTCAGCTCAGATGTGAGAG ACGC[G/A]TCTGTGACAGGAGCCGGTACGTGTCTTCAATCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70	T	C	AACCAGATTT TCTCAGGCCT	ACAAGAGGGT TGACAAAAGA G	AAAGATATAAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTAACCAGATTTTCTCAGG CCT[T/C]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCTCTGTATATAACCA

EST		A				Sequence
EST13278 2a	51	A	G	CTTTCACCGAA CAATATTTTAG G	CATATTCTTGG GTGGTGAGAA G	TTCGCAGAACGTTTTACAAGCTCCAAACCTTCACGGAACAATATATTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCCAAGAATATGACAGCTTG
EST132820	99	A	T	CCACACATTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT GG	GCTCACTAGATGAGCAGCATTGACCAAATATTTAGATAATACCTGTTGGGAAGTGCTGAATTACTAGCC TGCCTGAGAATCCCACACATTTCCAAGA[A/T]AACCTTCCTCAAATTTCCATCTCCCATCAGA
EST13290 9	39	A	G	CAATTTTTAGA AGTTTGGGTTT CTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACTTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTTG
EST13518 2	45	C	G	...	...	GAAACATCCTCCAGTAGTATTGAGGTTAAAATGATTCAGCATTA[C/G]ACTTTAAAAATTACCTCA ATGTTCCTCGGAGTCGTCCATAGTTTAAAATGACTTCTGCACCTTCCTTATAACCTTGATTG
EST13522 8a	66	A	G	...	...	CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCGATCCCCCACCCGGCCAGTGTCTGGAGAC[A/ G]GTTTTGATTGTCACAACTGCGAGAGGTGGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T	C	...		CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGGAGGTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C	G	...		AAGATTACGGACCCATAAGAACTGCCCCCCGACCCATACACACACAATTTATAGCAGGTAAAACCAA CTGAAAGGAACAAACAAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A	G	...		CCTCAACCATCTGTAACCCGAGCCC[A/G]CAGTGACCGGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A	G	...	GGAACAAGTC	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTCATAAAGTTAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGGAAGTCATCTGCTAAAATGACCGAACAGGAGGGTAGGGAGG
EST14221 5	42	T	C	GCATGCTAGA CAGAGGCATT	AAAATATTTTT AAAAGA	AATATCAATGCATTCTTGTTGGCATGCTAGACAGAGGCATTA[T/C]TTTGAAGATCTTTAAAAAT ATTTGACTTGTTCCCCCTTCACACTCATTTAAATTGT
EST14812 2	50	A	G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGCCTTTTCTAACATTTCATATCAGGTGAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128	A:T		CATCACCCACC GTACCGGAA	CGGGAAAACA ATACTGGTT	TTTGCTTCGGCAATACATAGTGCGCAATGCAGCCGTGAGTTCGGCGCGTCTCCCCACTGAACCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCATCACCCACCATACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA

EST	Pos			5′/3′ flank		Sequence
EST15420 6	109	C	A	---		TTTTAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTAATCTCTCCCCTTTGTCATCATAATCATATAGCCAAGGGACT[C/A]GGAATTTGGCTGCTTCAAGTCATTCCAAAACCTCTCAGG
EST15700 6	48	G	C	GGA / GAAAAGACAA AGACAACAGA AGACAACAGA / GGAATAGCTGA AACAGAGATA TTATTCTC		GTCACCAGCACTTTATTAAGACGTGAAAAGACAACAAAGACAACAGAGGA[G/C]AGCAGAGAATAATATCTTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCTTGATCTGATGTAGTA
WI-16739	57	G	A	GGTTTTGCCAT CACAAGC / GATAGTTGATG TTCATTATTCC CTATAA		AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC[G/A]TTATAGGGAATAATGAACATCAACTATCCTACACGTAAACCTAAGTAAGACCAAATTGCCTCCAAGT
WI-16782	96	C	T	GGTGGGGAGTCT CACTGTAAGG / CTTCTATCTTT CTGTTCCTCCA TC		CTTCTTCCTTCCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGACCATAATGGTGGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAGAAGTTGGGGTGCTGATGAAATTGTGGGG
WI-16783	64	A	G	TCCTGAGATGT CTTTTACCTGA G / CTGCTTGGTTC AATCCTTATTA G		AAAAATGTAAAACTTAGAGGTTGCCTCTCTTTGTGTCACTTTCCTGAGATGTCTTTTACCTGAG[A/G]CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58	T	C	---		CAGGACTTAAGGTCATTTGCCTGGAAGACTTTAACTAAAGGTCAGGCAACATAGGA[T/C]TGTGACAGCACCACTGGACCAGGAAGTGCTGAAAATCGTCACACTAGCGTGCCCAGCCCCTTTTTTCCTGGCTGCTCTGCCTCCCAGAGC
EST16088 8	89	G	C	---		GGTTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGGATTCTCATTTTGAGAGCTGTTTTGTCAGCCTTTTCCAGAAAAGGCCGGCTC[G/C]GGGTTTTCTGAACCCTCTATGGGCATTTTTAGAAT
EST16089 9	96	C	T	---		CGTCTGAAGTTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCCTGCTCAAATGCCACCTCTTCCTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGAGCCATCCCTCGCCCCTTTCTTTGCT
EST16100 1	24	C	G	---		ATCCCAGCTGTGAAGGGACCAGGAG[C/G]GTAAACACAGTCCATTTATAGGGTGTGCACATTCCCAGGGGCTCCAAATAATGCAACATTGTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAGTCACTCCAGACAGGTTGGCTC
EST16104 9a	83	A	G	---		TCTTTTAAATAACCCACAGACGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAGCTGGTTCCTCCAGGGA[A/G]TTGGCCCCGAAGCTGGTCACCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	---		ATGGTATAACAAAATCAGTTCCAGGTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAAACAACTAAAACAACCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA
EST16118 0a	32	C	G	---		ATGGTATAACAAAATCAGTTCCAGGTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAAACAACTAAAACAACCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA

ID	Frag1	Pos	A1	A2	Frag2	Sequence
EST16151 2		53	C	T	---	AGCCAATTCAAACGAACTCTATCAAAAACACACAAAGGCCTAGAGGAGGAGATTA[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6		54	G	A	---	CATTGGTTGGGTAGGGAAAGATAGTAGTGTGCAAATAAAATGGTAAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b		59	A	G	---	GCAGGTAAACTGTGGTTCACAACGTATTGTTCTTTCATAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTGCTCCTGGCCCTTCTTCGTTCATATTTTATGTCTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a		28	G	A	---	AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGAGAAAAAGTCAGCATCATAAACCACATGGGTCACATGCTCACGCACATGGTGTC
EST16229 2c		52	T	C	---	TGTGAACTCGAATTCGCTTGTCTCCAAGTTCATTGGGAGT[T/C]CCCTGTGTGCAGCC CTTGCCCAGTTCCACGAGGCAGGATACTCCACTAGCTCGATTCAGACAGGCAGAGGCTGCA
EST16229 2b		45	T	C	---	TGTGAACTCGAATTCGCTTGTCTCCAAGTCCTGAGTCACAGTTCATT[T/C]TGGGGAGTCCCTGTGTGCAGCC CTTGCCCAGTTCCACGAGGCAGGATACTCCACTAGCTC... CAGACTTTCCTCACACCTCAGTTGGCTGGAACTGGGTCACACCTGAACTATCATTGGCAA
WI-16816	GGAGGCCATTGT TGGGGTTA	124	A	G	GCCTAGATTTT GTTCAGGACGCAG	AGGGAAATGGGTCATCAAATTGCTTAAGGCCAGACGAGCCAGCCATTGTTGGGGTTA[A/G]ACTGTGTCC TGAACAAATCTAGGCTC
EST16269 5b		49	G	A	---	GCCACTCTCGTGTGGCTTGCTCCTGTCCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGGTCGTGCTGCTCCACTCTCTTCCGCCGCCGTGGGGCCTCACCACC TCTTCCTCCTCAATC
WI-16824b		83	G	A	---	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	CAGCTTCTGAC TTCTTCATAAG AA	47	T	C	TGATGGTGCTG CAGCTGT	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTT[T/C]GTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGGTGGGAGC CTTCCATTATGGGAATA
EST16445 3		96	T	C	---	TTGCTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACTT[T/C]GGAATAAAGAGCATAAAACGGAACAGTAACATCA
WI-16857	CAAATAAGCA GCTAATGGCA A	47	G	A	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACAACACACAACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATTGTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA

Clone	Pos			Seq A	Seq B	Full sequence
WI-16879	79	C	T	GATACAGGCC ATATTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99	A	G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCTTCACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC[A/G]GCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G	A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTCATCACTACCCGGGGAGAGCAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT CTAGGCAGTG GG	TTTGTTGTTGTTATTGCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCATTTGGGCCTGAACCAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAACACCAGCAC[C/T]GATGCCACTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG[A/C]CCA CGGGCAATCACACGAGATG
WI-16947a	58	C	G	CATGGAAATA GGCCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGC[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACACGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAAAATGCACACTACATAACAACCTAATAT[T/C]CTTAACTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[T/C]ACGGCTGG AAATCAACATGCCTCTTCTTCTGTGAAGTTGTCAGCAGGCTGAGTCAATCT
WI-16992b	60	T	G	...	CACATTCCCTT	AAATACATGGTGTCAACCTCAGCTAAGCTACCAGAAGTACACTGTCGCCCCTCATCTGAGA[T/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA
WI-16992a	46	G	A	AAGCACCCAG AAGTACACTG TC	CACATTCCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTC[G/A]CCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA

ID	Pos	Alleles		Seq 1	Seq 2	Sequence
WI-17010	23	T	. C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAGAAAAGCCATG[T/C]ATGACATTCAAAACACCGTATTATTAGAAGCTCATTTAAT GTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAGTGATCAACCTAGA GGTTCCCACG
EST17127 9b	74	C	T	CACTCGGCAC AGACAGAGT	GGGAGGGCCAGG GGTG	ATTCCGTCTCCAAACAGCAGCCATCCCCCCACGATTTATAATACACTCGGCACAGA CAGAGTC[C/T]TGGGAGCCATGGGCACCCCTGCCCTCCCAGGCTTCCTAAGTAACAACT
WI-17040	94	T	C	AATTCTCTTAT CATCTCAAGCC A	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCATTAAATTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAATTCTCTTATCATCTCAAGCCAGT[T/C]CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTCC AAATCTTTCTCATATTGT
WI-17044	47	G	T	GCCAAGGGAT TAACGTATAG G	GGGGATCCCCT TGTTTAAGA	TTGTTTTGTTTTGTTTTCTCCTCCTGCCAAGGGATTAACGTATAGG[G/T]TCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAATGGCAGGGAATCGAAT CAAAAAGAAAAGCAAGTG
WI-17021	62	T	A	TGGACTTGTCA GCCTATAACT ACTC	TGTAGAGTTAG TGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAGTTGGACTTGTCAGCCTATAACTACTC[T/A]G CAGCTGCCACTAACTCTACAGGCACAGTAACTACACTTATACAGGAGCACATGCCAAGTGCCTGG GAGGGTGCCAATAAAATCAA
WI-17065	9.0	T	C	CCAGAAAGGA AAAGCATAAA CTT	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTA CCAGAAAGGAGGAAAAGCATAAAACTT[T/C]AGGATTTCATTGTCTCTTGGGT
WI-17066	32	A	C	TGTACAGCCA ACATCACTGTT T	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAACATCACTGTTT[A/C]ATTCCAGAACATTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATTCCCTGTAGCTTCCTCATAGGCAATGGCAACTGCTGATC.
WI-17074	86	T	G	...	...	TGCTGACTGTCATGACTTAGTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCACTGTTCCAGCAT AACCTCCTACACAGGCCTTT[T/G]CTACATAGGAGTATATTTGGCCAAGACTCACCACTAGAAGTGATT
WI-17104b	108	T	C	...	...	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCGTGATGCTTTGCGAGCTTCCCATTCATTCCA AATCAGAAGCAGTCAGTGCCCGTGGTTTCCAGACGGCTT[T/C]TCTCTTTGTTAAGAAATTA
WI-17114a	37	T	C	TTTCCATCAAG GACTTTGTTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTT[T/C]GTCTCTTCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAAGAAGACTGCAGCCAATCAGAGTTACAT GGGA
WI-17150	76	T	G	GATGAAATTC AGATAGTCTTC CTCTTT	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTCTTCCACATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCTCTTT[A/G]CATATCTTCCAGGATTCTGAGGAAGGGCCTCCTTTGTCTGCTCTAATTT
WI-17163	43	A	G	CATTTCTTTGT AAAATAACAA TAACGTT	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCCATTTCTTTGTAAAATAACAATAACGTT[A/G]AGGCAAAAGCAAGATTCTG TAAACCAACATTGAAAAGGGGACACAGGGAGGGGCAGAGGGAAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

ID	Pos					Sequence
WI-17178	127	T	C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCCCTCCAATTTCATTCATTAGCTATGATGGAGTTATCAGTTCATTTCAGAGCGGAATTACTGG GGCGAGGGGGGTTTAATATCCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C	G	---	---	TCATGGACATCCTGAAGCAGCAGACACAAAATATAGAGAATCCTGCACTTCCCAAGTCTCGTCGCACAG GCTTCAACAATTAC[C/G]AACATCTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T	C	CACAAAAATA TAGAGAATCC TGCA	---	TCATGGACATCCTGAAGCAGCAGACACAAAATATAGAGAATCCTGCCATTTT[T/C]CCCAAGTCTCGTGTCGCA CAGGCTTCAACAATTACCAACATCTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G	C	TGTTCTCTAAA CTTTAGATATC TGTGGAA	CAAGAAATAT ATATTGATTC TCCCA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCAT[G/C]TTCCACAGA ATCAAATATATATTTCTTGGTGGAAATTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT TAATATTCTTG
WI-17149b	79	T	C	---	---	CAGGCAGTTAATGTCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCA[T/C]GTGTATGAACTACAAAAGGATGGGGAAAAGAACACATTTCCTCACA
WI-17149a	48	C	G	CAAGGTTTGA AGGAGGAACA CATGA	CCACGCACGTG CATGA	CAGGCAGTTAATGTCTGACATAGTAACAAGGTTTGAAGGAGGAACATC[C/G]TCATGCACGTGCGTG GAAACCCAATTGTCATGTGTATGAACTACAAAAGGATGGGGAAAAGAACACATTTCCTCACA
WI-17197	67	G	A	GCAGAAGTAG CTGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTGCCTGGGCTGGACTCCAGCAATCCTCTGCCTCAGCAGAAGTAGCTGGGCTAC[G /A]GGTATGCACCACCTCACCCTGCTATCCAGTTTCGTTAATAGAATATTTGACTTTTAGATGCGCA
WI-17198	38	A	C	TCCCCCTTGTC CCCTAGTTT	TCCATTTGTCC ACTGAGAAATT	TGTATTTCAGTACTTTCCTCCCCCCTTGTCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTGAATTTGAATACAGATACATCGAAGATATCTTACAAGAAACAATGCACATCC TTC
EST18753 8	27	C	T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACAACAACTGCCACCAGGCCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C	T	GCCATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTAAAACATAACCAGATGCACCTTGGTTTTTACATTCTCTGGTTGCCATTCAGTCTCAAAGT AAACAC[C/T]GGGAGCATATGATAAAATCGTAGTTTAAGGAAGCCATAGCACTTACAGAGT
EST19067 2b	41	A	G	---	---	ACACAAAAATTTACCATCCGTGACCATTAAGGGTATAGTTCA[A/G]GTGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCCATTCATCATCCATCTCCGTT
EST19067 2a	40	A	C	CGTGACCATTT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTAATG CA	ACACAAAAATTTACCATCCGTGACCATTAAGGGTATAGTTC[A/C]AGTGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCCATTCATCATCCATCTCCGTT
EST19125 8	28	A	G	---	---	CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGCATACAATACAGTTATTGTATTGGC TATTCACAATTTACAGTAGTGTTTTTCCCTCTGAAAA

ID	Pos			5' flank	3' flank	Sequence
EST20824 8	115	T	G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A	G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGTCACATCCTCTCAGAACTTCTCAGCCT[A/G]TAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATCAGACGGGATGTGAGTGGGACCA
EST21904 b	128	G	A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T	C	GAAGATCTGT CTGGCATTCTT T	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAAATTCAGAGAGCTCAAGTCACCATGTTGCTAAGAGAAGAT CTGTCTGGCATTCTT[T/C]GTGGGGCTGTTTTCCAAGGCACA
EST22197 2	78	T	C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTACAAGCACCAATTATTCTGCT ATTCCTGCCATT[T/C]ACCGCCATCCTTCATGGTAGAGTACACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92	T	C	...	...	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCACCACTGTAAACAG TAGCATTCAATGGTTTTTACTCTAT[T/C]TGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9b	54	A	G	...	...	TTTTCCATGGATTAGATCATCATCTTTTTATTGAGTTATAATA[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9a	41	T	C	GGATTAGATC ATCTTTTATT CGAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCATCTTTTTATTGAGTTATATAA[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22319	19	A	C	...	G	TCGAGGAGCTCTGAGGAGC[A/C]CACCAAGGGACGTGTGTCCCAGGGCCACGTGCAGGCAAGTGTG GTCCAACTCCTCTCCCTTTACAAAACTCCAGCCTCCAGCCTCCACCACCACAAACACTGGCTGACAGGCCTTCT TAAGCCTTTTTAACTGT
EST22433 c	103	A	G	AAGACATGTT CACCAAGTGA GAA	CAGCTTCAGCT TAACTGACAGA CTGGGAGCTTGACAGA G	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCCAGGTACACATGGAAAAGACATGTT CACCAAGTGAAACCAATCTAACCAGAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAATT CTGGGAGCTTGACAGACTG
EST22657 9	71	A	G	AGTTTCAGTTT AAATGGATCC TTATCTGCACA T	GCATGAATTTT	TATCCATTTCAAGAAAAAAAAAAAATGACTTAAAAAAATACAATTCTATCCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAGAAAAAAAAATTCATGCAAACTGAAACTATGCTTT

ID	Pos					Sequence
EST22993 5b	71	T	C	ATCCTTTGTT TCTACCCCC	TTGCCTGTTAA TTTGACTGTAA TG	GCCTTTTATTGTCTCCTTTAACATCAAAATGTTTATAACACACTGATCCTTTGTTCTACCCCCA AT[T/C]CATTACAGTCAAATTAACAGGCAATATAATATAGGTCTAACAGAATGCTTGCATT
EST23021 0	108	T	A	...	...	TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTGTGTGAGGTTAATTTTATTAATCTTTGGCCTT[T/A]ATGGTTTGACAGTTGTGTCTTTCT T
WI-17387	55	C	G	CCTTTGCAGAT TGAAGAAAAA	GCTTTTGCCTA AGATTAATAGT AACTACT	ACAGAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAATCTTAGGCAAAAGCCATTCTTTG
EST23669 1	101	A	C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAATAGATGAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGGAAGGGACGGCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733 9	31	T	G	GGCTGTTAGTT TGTTTTGTT TT	TGCACTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTTTGTTTTTCCT[T/G]TATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCCTAGAGAAAGATATGAGGCCCGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83	A	G	GTCCCGTGCCG CCAG	CCAGTGACGAG GCGGA	CTGACACGTCCCGTGTGCGGGGGTGTCCATGTGGCCGGTGTGTGAGTGAGACTTTTTACTGCGTCCC GTCCCGCCAGCCCTT[A/G]TCGGCCGCCTGCCGCTGGCCTTGTGTATTTCGTCTCGTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55	T	C	GTTGTCCTAGC TAATGAATGC A	AATTATTATTT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAATGCATTGTTGTCCTAGCTAATGAATGCA[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAGAAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C	G	...	...	TCTTTGATACAGGTAACCAGTTTGTAACATATTATTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAAATGTCAACATCAGGATTTCTTTT
EST25356 3a	26	A	C	...	...	TCTTTGATACAGGTAACCAGTTTGT[A/C]ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTT
WI-17581c	99	C	T	...	...	GGGTGACGCTCCAGAATGGGAGACAAGCCAATTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAA[C/T]TTAGGCGCAATTTACATTGACGGGTCATGC
WI-17581b	86	T	C	ATTCAACATT ACTACCAGTT ATTTGATAA	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAATGGGAGACAAGCCAATTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A	G:C	ACTTCCTTGTG TAAACACTCC C	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCTTGTGTAAACACTCCC[A/G]ATATTGTCGATTTCTAGCTATAAGAATGGGGCCACTAAGTGGGTC

ID						Sequence
WI-17623	46	T	C	---		TGTGGTTTAATTTAATTTCCCATATAATTAATGGTGGGCACATT[T/C]GCATGTGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46	T	C	---		ATTTCATACAGAGATACAAAGGCAACTATGTGCAACAATCTGA[T/C]GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35	C	A	ATACAAAGGC AACTATGTGC AG	CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG[C/A]AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69	G	C	---		TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGCATTTGACAGGACAGCAGCAGTAGTTCAAGC AG[G/C]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A	G	---		TACTTCAGTTTAAGGCAAATTCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCAGAGACACC GTAGAAACACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101	C	T	---		CAAAGGATTTATTTGTTCCCTAAAAAGTAAAATCTAGAAAAATAGCAACCCACTGCAAGAGAGTT CTATACTAAAACATTTCAATCATTCTCTCTCT[C/T]TCACATGGTACTCTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33	G	A	GCACTTTGCAA CAATTTAATA ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTGCACTTGCAACAATTAATAATTTATC[G/A]CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTCTGTTACACATTCTGTTAACAGAACCCATACATT GGTAAAATTCATTCT
EST27662 4	51	C	T	CACATTCTGTT CTCCAGTCTTG	TTATGGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAGAAAAGGCCAGTCACATTCTGTTCTCCAGTCTTG[C/T]AGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTAGGAATGTTC
EST27788 3	100	A	G	---		ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAAGGAAAGGCAGGCAAATACAT TATTGAGCTGAAAACAACTTACACTTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58	G	A	GGAAGTCATC AGAACCCCAC	GTGCAGAGAGG TACTCCCAAGTA C	TCTTCTAAAACTTCCTTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCAC[G/A]GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58	G	A	AATAAATTTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTCCCCAATGTAAACAATAAATTTCAATCTGTCACACAATC[G/A]AAATG GATAAGGCCTTCTTGACAAATTTCTGCCACCTCCGTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37	T	C	---		TCCCGCTTCCAAAAGCTTTATTGGCAAATATGCTCTA[T/C]AAAAGAATGATCAATCGTTGCCTCT AAGTCAATGAATGAAGAGCTGTGTCCAGGGACCACCACGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

ID	Pos						Sequence
EST284837	31	T	A		GGAGTAAAAG GTGTTTTCTT TTAAA	TTTCTCGCATT TATTTTTATAC CA	CATTTGGAGTAAAAGGTGTTTTCTTTCTTAAA[T/A]ATGGTATAAAAATAAATGCGAGAAACATTAAC GGAGAATGTACAGACAAGACGAAGACATGAGTTTGTTCTGACGTGTGACACATTGGTGAAA
WI-17724	50	T	C		TGGGCCCTCCC TGTC	TGGGTTGGCAG TGTCC	AGAATTGGTCTAGTAATCGTTCAGGATTCGGTGATGGCCCTCCCTGTC[T/C]GGACACTGCCAACC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68	T	C		---	---	TGAGCCTGGGGAGAAAGACCACAGAGAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG T[T/C]CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39	A	C		GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAGAAGTGAAGTGCTATT[A/C]GTTACATCATACCAAGTGTACATA CTGTTCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST290415b	53	G	A		GGAACAAACA CATTAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACAACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAAACAATACCCCTTTATTTTTAGCCATGAAAAC
EST291284	58	A	G		---	---	CTTTAGAAGGGACACCAGTCTTGTTGGACTTAGGGCCTACCCTATTCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCGTCTGTAAGGACCGTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGCAGATGA GTTTTGCTGGGGACACT
EST299123	103	C	T		TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTTATTAGGTATCTGCTGTTGGGGGGTGGGGGATTGTTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAAGAATGAAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST299368	121	G	C		---	---	TATTGGTATGCTTAGGAGGAAGATTCTGATTAGAGATATTAAATCTTAAAAGTTAACTCACCATGAAA TTAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST302232	99	A	G		---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCCTCAAGCATTTATTCTTCTTTGAGTTACAAGCAA TCCAATTACACTCTCAAGTTATTTAATATTCC[A/G]GGATTAATTTCTTCCTAGTTCAATCTTGGGA GG
WI-16260b	86	G	A		---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAGACCCAGA GTTCACAATATAGGTAGC[G/A]ATAACCAGGTCTCACTTTCCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G	T	A	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA[G/T]ACCC AGAGTTCACAATATAGCGATAACCAGGTCTCACTTTCCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30	G	A		ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAAACAGGAAATATTGTGCTTTCTTG[G/A]GTTGTTGCTTCTATAATGTTCCAGCTTCAAAT TCTTTGCTTCTCTATACCCCAATATCATAAGAATT TTCTTCCTCTTGTTCAAAA

Marker	Pos	A1	A2			Sequence
EST31951 4	87	C	T	GGGTTGTCCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGAGACTGAAACATTTCACTCTTTAGCAATGACA TCGGGTGTCCAGCCAACA[C/T]GGAGGTGATTTTGGTGGGGAATTCTTATCACAATTATTCT
EST31968 8b	95	T	G	...	...	CGAATTTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGGATTTTCTGCT[T/G]AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T	C	GCGGGGTTACTA TAAGTGCATTT T.	TGTAAGAATCA GTGGGGCAGTT	CGAATTTGTCTCTCTATTTGTGATTCTAGTAATCCTAAAAGATTT[T/C]ATAATGGGGATTTTCTGCCTTAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C	T	...	...	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCAGGCGCCCATTGAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A	G	...	...	AAGGCTTTCCAAGCATTCCAAAGGCACTTGGGTGTTGTGCTCTCAAGTTTCTGGTCCACTGCAGCCCC[A/G] TTCTGTATTAGGGAGCACCCCAAGCCCAGTAACAATATGGTTCTTGCAG
WI-17800	29	C	G	GGGAGCACAA GAGAAACTCA	TTTCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCAGCACAAGAGAAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGCCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T	G	CCTAAAGTCTG GGATGACTTTC C	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCC[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAATTCCAGCTAACTCCAAGCTGAATTAAATGTTCATTCT
WI-17860	121	T	A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTA TAGTGTCCAAAGATAATTAATTCTTGGTTTAAATCTTTGCCAGCAAAGCAAATA[T/A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A	T	TTTTTATAGCCT ACTTCTCAA ATTGTT	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTGTTTATAGCCTACTTCTCAAAATTGTT[A/T]TTTGTGTGATTAGTGACAACG GGGGAATCTACAAATGCTCACACACAGTAAACTACCA
EST33301 4c	80	G	A	...	...	GAAAAAAAGTCAAATGTGTTCCCTTATGGGTGATGCCACCATGCCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGAATGCCAAAGAGTATGG
EST33301 4b	63	G	A	...	...	GAAAAAAAAGTCAAATGTGTTCCCTTATGGGGTGATGCCACCATGATGCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G	A	AGCGGTGGTTTT CAATACTAAA CA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTTCAATACTAAACA[G/A]TGTAAACAATGCAAATATT TAACAATAAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAATACTTTGCAA

Marker	No.	Allele			Sequence
WI-17904	50	A|G	AAAGCATGAC AATAAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAAATGAACAC[A/G]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAAATGCAGTTAAAACAACAACAAAATGA
EST341495	69	A|G	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACTA ATAAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTCATTTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTCATGAAAAAAGCAGTAGTTCAGC TTACAAATCACACAAGT
EST343438	95	C|A	---	---	TGGGAAAACATAAGTTAACTCAAGAATATATTCCAGTCTTTATGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTGC[C/A]TACAAAGATTAAAGAAACTTACCATCAAACACTTC CAGTGCATCAA
WI-17982	98	C|T	GGACCATATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTAATGGAAGGAACCACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGGACCCATATGATATATAAAGC[C/T]GGAAGGAGGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A|C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTATTATGATAAAAACAACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCAACCACTGTCCCTGTAATGTA[A/C]TGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A|G	GTAGAGGCGA GAGGGAACAG	AGGCACATGG CAGC	CCCATCCAGAAACCCCAGTGTGATGGTGGAAGCAGCATGAAAACAACATCTCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCCATGTGCTGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C|G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24	A|C	---	---	GCCACTGAAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAAGGCAGTGTTGATGCTCCAGGAT TCAAAATACTTAATCA
EST351648a	57	A|G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCTTCAAGCACAGCCCTGCCCCC[A/G]TCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCCTGGTTAGGTGCTTCTTGTGACATTCCTCTTG
WI-18052b	67	A|G	---	---	AGCGAATGAAAAATGCTACTACATAGGCTCCCTGAGTTCTTCATGTACGAATCTTGGTTACACATCTTAG[A/G]ACAGCAGAGCTGCCTGAGGGAGGGGTTGTTGTTTAATGTCGTATGCATGCTGGCC ATGGCCCATCCATGCTTT
WI-18052a	50	T|C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACTACATAGGCTCCCTGAGTTCTTCATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGGTTGTTGTTTAATGTCGTATGCATGCTGCCAGTAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G|A	GGGAGTGGGG GGAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTCTGCTGAGAACAGAAGGGGTCAAGGGAGTGGGGGGAGTAAAA[G/A]TGGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

Marker	Pos	Allele	Allele	Sequence
WI-18064	54	G	A	CAGCTGCCAATCATCTCTCAAACCCTGTGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCACAATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGGTGCCAAACTGGGGTACCTGGGAGGCAGAAA
EST35347 2	97	T	C	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGGAATTTTGTGTATCTGGCTTCATGGGGATGCATAAAAATTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCAGGCA
WI-18070	28	A	C	AAACCCACTACTTACTCAGAGTGTGTAT[A/C]ATATTAAACACATGAAAGATATAAATCTTAGAAAAAACCTCCAGTTCTTATTAGTTTGATATTTTCTGTACTCAGAAGCATTTAGGTTGCAAAGGATATAA
WI-18080c	80	C	T	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAAAATCTACTATGCCGTGTTTGACTTTTAT[C/T]TCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	G	A	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAAAATCTACTATGCC[G/A]TGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T	C	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTC[T/C]TTGTAATTAAAATCTACTATGCCGTGTTGTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63	G	A	GTGGGCATCCTATAAAGCAGCCATGTGTTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A]TGGCTTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCCAGCTTCTGCAGTCTAGCTTAGGGAGAGGTGTTTGAA
WI-18115b	71	C	T	AACTACATAGTAGTGGTGCCTGCCTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCCTTC[C/T]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAAGGGGTGAGTCAGT
WI-18115a	70	C	T	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCCTT[C/T]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAAGGGGTGAGTCAGT
WI-18136	78	A	G	TTTTGAGAAGCACTCTGTAAGGCAGGATGCATTCAAAAAAATGGCTTTGAGGATTAATCTCTCTTTAGGTAATTTGC[A/G]TAAGAACAATAAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115	A	G	GGCAAAATATTTTACATCACCACTGGAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCGTAGAGTGTGCAGGAGGAAAGGTGTTATCCAAGCAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGCAACAAGCAGAACTCGGTGGGTAGAGTGGA
WI-18190b	26	G	A	TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAACAAGAGGATGAAGCTAATCATGGAGGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA

ID	No.	A1	A2	Left	Sequence
WI-18190	62	G	A	---	TGAAAGAAGTCGCACACAGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGAGGACACAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A	C	AAATATATAC AACACTCCCTT CAGATC	GACAGTGAAAAACATTGAAAACACAACACAAATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAACGTA TGTGTTCTTGAAC
WI-18215	78	G	A	AGCAGAGTTC CTGCCCTC	ATTCATACAAGCATTTCCTGAGTACAAACTAGGGGACAGGGTATTTCACAAAACAAATAGAGCAGA GTTCCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGGAGGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60	T	A	TGGTTGTTGATT GTGATACACTT AA	CATTTCCGAAATCTGATAGTTAAAATATCCCGTCTGGTGTTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAACCTTTATTTGAAATTGAAGTTTTGCTCAGAAACTGGGCGCAGAACTTTTCACATTCTG AC
WI-17892	76	T	C	GGAAAACTTG AGTTTGAGATC ACA	TTTAAAAATGCTTAGATTTTCCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C][C]TGTCTCTCACTAGTCTATTCACTTCTGTGTGGGCATTCGGCCAGAAGTGGC
WI-18242	30	G	A	CCCCAAATGTT TACTGTAACAG AATCGTAACA CTTTC	AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTTAGCAAAAAT TGGATGCCACAACTATCTCACCATTCCTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C	T	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T	C	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATCCACAT[T/C]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C	T	AAATAGGAAA TATGGACTATC TTCAAA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCACAAATGATGCATGAATCCACATTCTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A	G	GCTGTCAGCTA TTGTTATTTCA AA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATTGTTATTTC AAAT[A/G]TATCTTCTGCTCCCTTTTCTGGGATTCTCATTCTGCATGTGTTATA
WI-18330b	66	A	G	---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAGAAATCAGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTGTGAT TCACA

ID	Pos			Seq 1	Seq 2	Sequence
WI-18330a	49	G	A	TCCTGTAAGA AATCAGGGAT AAGA	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGTAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTGTAGGCAGTGAGTCAGGACTATGCAAAATAAAAATAAAGAACCATAAAAATAAAATATTTTTGTTGAT TCACA
EST375645	85	T	C	AAATTCAAGC CATCTACAAA AGA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCACATAACAGGCTGGAATTGCTAGTGGTTAGAATACTGCATGTTATTAAGCTAAAATTC AAGCCATCTACAAAAGAT[T/C]TCTCATTGAGGCCTCCATAGGCTGCAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G	A	AAACAGCTTT CGTTAGGCTAG TT	CGCATACAATG GCTCAGC	CAAAGGGATTTATTACCTACAACAACAGTAAGGAGGACAGCTGGGCAGTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAAACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST376246b	102	G	A	---	---	GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCCTCTGCCGTGCTCTCTGGCTCTTCTCTGGACG[G/A]TTCATTCTACACATGGCTGCTTGCGGTCC TCTGACCTCCCATTCC
EST376246a	58	C	T	---	---	GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCCTGCAGTCCTCTGCCGTGCTCTGGCTCTCTGGACGGTCTCATTCTACATGGCTGCTGCTTGCCGTCC TCTGACCTCCCATTCC
WI-18357	89	C	G	CCCAGCCCTTA GGCATCAA	AGACTGAAGAT GA	AATGTTTTAAAAAGTCCTACCGGTGCTGAGGTGGCCATGAAGCCAAGCCCATGGAGAGACATTTCAGA TAATCCCAGCCCTTAGGCATCAA[C/G]TCATCTTCAGTCTTGAGTCCTTCCAGCCCAGGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A	G	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTTCGTGA[A/G]GTGTTTCCTGATACA CGCTGACGTTTCGAGGG
WI-180126	113	G	A	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTTC[G/A]TGAAGTGTTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C	T	GCCACTTTTGC CCCTT	TCAGCGGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTT[C/T]TGAAGTGTTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTT[T/C]TCAACTTTCCAGACTTGGA AGATCCCCGGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTTCGTGAAGTGTTTCCTGATACAC GCTGACGTTTCGAGGG
EST383904	75	A	G	GCAAAAAGGA GCTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATTCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[A/G]ATTAAGTTTATTAATCAGCTGACTTAGCATTGGGAGATTATTCTGGAT

EST						
EST38512 7	91	T	G	TGACGGATGCC AATACTTCG	CACTGCGACTCT GGGAAGC	TAATAAAAACTGACCCAATTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCG[T/C]TCCCCCAAGTCCTAACAGAATGGTATATTCCTCTGGAAAA
EST38519 0	24	C	T T	CCTGCACCTCC TAAAAGATCT T	TCTGTTAGGAC TTGGGGGA	CCTGCACCTCCTAAAAGATCTTTT[C/T]TCCCCCAAGTCCTCGTTGCTGCTCGTTGATTTTTTGTCCTTGAGAACCTTG AGATGAACGTCATCAATGGATTGTGCTGCTCGTTCAGCTTGATTTTTTGTCCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66	T	C	GAACATCCCA TGTTTCTGTTT AA	AGGGAAGGTA GTATAACACAT CA	AGTGGTCAAATGTAAAACTAATGGGGACACCAAGCCTCAGGAAGAAGAACATCCCATGTTTCTGTTTAA[T/C]TCTCTTATGTGTTATACTACCTTCCCTTCTTTATACACATAGATTTCCTTAATTGCAGC CCA
EST38616 9	101	C	G	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGCC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCCAGAGTGGGTGCCTCACGCCGGGCCCGTGG AGTCTCCCGGGCCCCCGCCCCTTC[C/G]GCCACCATCCCATTCCTCCAGGGG
EST38652 8	59	T	C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCCTTGCTGCGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTTTCCTTTCATTTTTGCAAGTAAAAAAATCAT
EST38654 5	42	T	C	AATGGTCATTT TAATATATCA GTTTTACA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGCAGGTTGGTTCCAGCATATA
EST38707 9	75	A	G	---	---	GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC[A/G]AGGCCAGCGGGGATGTGTGCCCCTCCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38759 2	86	A	G	TGTCTCCCTGA GGGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGTATTCTTCACTAGAGGGGGAGGAGAATCACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[A/G]CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATTCTTGCC TAGCAGCACC
EST38775 1	40	T	A C	AATCAATAGG AGAGGATTGG C	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAAGAGAAAATCAATAGGAGAGGATTGGC[T/A]TTGAATTCAGAGGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCTCCAAATGCCCCTTCATGAGTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91	C	A	TGTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT	CACCCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA[C/A]AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98	C	T	CACGAGTAAA AAGAAACTCA TGAC	GGAGCGAGTCC AAGGAGAA	TCTTTACTGTGCTTACAACTTTCCTCCAAGTTTGCGGTGGTTTCCATATTGTTATTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC[C/T]TTCTCCTTGGACTGCTCCTCTCCCCCAATCTCGAT ACCGACTGCACTGTTG
EST38865 2	72	T	C	GCTGTAGAATT TGTGTGCGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC[T/C]CTGTGTCCTCCGTCCTTCCCCAAATGAGCACATATGCAGGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

ID	Pos					Sequence
EST38878 9	47	T	C	AAACATCATT ACTAGCCTAA ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTACTAGCCTAGATCCTAA[T/C]TGAGGAGGACATGAGAATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTCTTGAGAAATGGGAAATTGAAAACATTCCC
EST38882 6b	113	G	C	---	---	TTATTCAATGTCATCTCACACATTCTTTATTTTTA[T/C]TTGTTTCACTTTCTCAAATATCGGATTGTTGC TCATGAGAATAATGGCTGGCACGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6a	35	T	C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCATCTCTCACACATTCTTTATTTTA[T/C]TTGTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAATAATGGCTGGCACGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATT TA
EST38909 5	47	A	G	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTCATTTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAAGAGAACTCTCACATACTGCTGGAGGGAATATAAATT
EST38911 9	85	A	G	GTTGAGGGAA ACTTATAACCT TCAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAAAACACTACACATCAAAACTTAGGAAATGTGGTTAGTGTGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCCTTGTTCACAAAACAACAGCAGACAACAGAGATTTCCAACTC CAGCAATGACAGAGGCTAGGG
EST38955 5	30	G	C	TGAATTCCCTT CACTGCAATCT GGGTGGG	CACTGCAATCT CACCCCC	TAAACATTCCCATTGAATTCCCTTGGTGGG[G/C]GGGGGGGGTGAGATTGCAGTGCTCAAGATAAA TATCACAAATATATCAAAACTTCAAATTGTCTATGCATCGACACTGACACATTGAGCCACAAACATT CCTTTCACAGGGACTGTAC
EST39002 0	42	G	A	GGACCCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCCCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACGCGGGGCTCCCCAGCTCGGGGCCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79	T	G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCTAAGTTCCGGGTCTTCCTCAGTCTGGATGGCTGGTGGTGGAAAAGCTTGGTGGTAAG GCCTAAGGAAT[T/G]GAGGGGCAGGGGCGGATGCCGCCGAGATGGTCCTGTAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90	T	C	TCCCTATTATT CCATGATATTT CTCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAAGTGTCATCACAACGCAACATATAGAAACATAAAAGAAATAAAGTATCCACCCTAAAAT CCCTATTATTCCATGATATTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69	T	C	CCTTTGTCCTC AATTTTTAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTCTTCATGTATTTTTCTCATTTCCTATCAGGTTTCTGGTCCTTGTCCTCAATTTTTAACACTT T/C]CTTTTTATATATAGGGAATTAGCCCCTTAAACTGTGGTACATGCTGCCAAAATTTCCTCCCAGTT
WI-16406	24	C	T	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAAGAGG[C/T]GGTTTTTTATTTTCTTTTTTAAACACATCTGGTTCTGGCAGC AAGTTATTATTATGCATTTAGAGCAATAGGTGCCCTGAA

ID	Pos	Alleles	Sequence (flanking / SNP region)
EST39236 0b	57	C | G	TCATCTGAGA ATAAACTTCCT GTCT — CATTATAGGTA CTGAGTCATAC ATTAAACA TTT — TCCTTTTTATTCATGATTGTTCATCTGAGAATAAACTTCCTGTCTCTAATTTCCAA[C/G]ACTATGTTTAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGTCTC
EST39294 4	63	G | T	CCTGAAACAG GGATGCC — GCACAATTAA ACATAGTACCG AGAA — CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T]TTCTCGGTACTATGTTTAATTGTGCTGAGCCAGCAACCCTGAGTTACCCGGCCTTTACCCCACGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72	T | C	GAGGGGGTTCAGA — AGAAAACATTCTGTCTGATCAGAGGAAGAGTGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[T/C]ACACTGAGAGGAAAAATGGAAAAGAAAAATGTTTGCATAAAGCTTTGCCTGACTCTCA GAGGGGGTTCAGA
EST39371 9	86	A | G	CATTTGGATTA GCGTGAGAGG — TGATTTGAGAC ATTTCACATTT TT — AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATTCCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTCTCAAATCAAATGCTTCCTTCTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23	A | G	ACAAGTGACATATCCAACCAACC[A/G]TCCATCCCACCTGTGCCCATTCTTTCCTTGTTCTTT AGAGGCCTTTCAGCTATTTCCTGTGAAGCAAACTGCACGAAGGCCTCCCCGTACTCCTCCCCCTGGAA G
EST39428 8	31	C | T	GCTCCCCACA ATTTTGATT — GGTCCCTTATG AAGCCACC GGCTGTGTGC — AGGTTCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCGGGTGGGGGCCTAGGTAATTCTGTTGCCTTTGGTCCACAGAGCACAATTAAAGAAGAGATCAGGTCT
EST39430 2	45	A | C	GGCAGAGGAA TAACTGATGTT ACC — CAGGGGTCGGGG GTATTG — AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTTC[A/C]CAATACCCGACCCCTGA CCCAGTACCTTTCCCCTCAGGCGGCCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117	C | T	CTACTGACAT AGGGACTTCA GAGTAA — TCCTGGAAAAC TGACATAAACC TTTCCAGGATTGTTCTCCC — AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAATAACAGGAACCTATTATAT[C/T]GGTTTATGTCAGT ACGTAAATCACTTTCATACCTGCCTACTGACAGTAATA TTTCCAGGATTGTTCTCCC
EST39465 2	80	A | G	AATGCAGGAG GGTGGC — CAATCTCGGCC CCTCT — ATGGTGTCATTAGAGAGGGCCACAGGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA[A/G]GAGGGGCC GAGATTGGGTGTTCAGGGCAGGAGGGTGGAAGACCAG
EST39501 0	81	A | G	AAAGATTCCT GTAGACATCT AGAACATTAG — CACTTGCAATT CTGAAGGCT — TGCTTACAACCCATAACCATAGGCCATGTGTTCAGACATTCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAATTGCAAGTTCAAACCAATTC
WI- 18387b	84	A | C	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTGGTGACCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAGTGTAAATGTGCGATG GCTATGTGTAGACATAAAGA

Name	Pos					Sequence
WI-18387a	57	A	G	CCTTACTTTGG	GCTAAAGCATG	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCATAC[A/G]TTTGTGGTCACATGCTTTAGCCATCACACATGTAACATTGACTAGGAGTCTTGTGAAAGTGTAATGTGCGATGGCTATGTGAGACATAAAGA
EST406019	78	A	G	GCGGTGGAACCT GAAACAC	TTCTTGGAAGA AAGGCGTC	TCCCAGGATGGTTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGAACCTGAAACAC[A/G]GACGCGCCTTTCTTCCAAGAAGGGCTGTGGCGATCAGCCACTCAAGG .....
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTCAGTGTATCACATCTTCAGGATAGGTT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTCTTCAGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTGTTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGA CA	AAAACTGATTT GTTAAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTAACAAATCAGTTTTTCATAGGCAACCTTTTGAAACATCAAAAGAAAATACAATATATTTTCACAAATTTCTCATCACTGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAGAATAAGGGAAAATGGGAAGAACAGAGTGAAATTAAAGCAAATCTTGGATTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAATTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTCAC TC	AGAGAGACAACAAGAAGAATAAGGGAAGAGAA[C/T]AGAGTGAAATTAAAGCAAATCTTGGATTCAGATTCCATTAAACAGGAAGTTCCTCAAAAAATCAAATCAAATCAAATGCTTATAGCAATGCTGAGAATTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	...	...	AGCTGATCAGCTGTCGTACTGTGTTTATGTGTGGCCCAGGGAAGCAAAAGATCAGACACCCTGTCCTAGACAGATTCAATGCACACAACAACAGGAGGT[T/C]GGGGGGTCACGGGGCGGGAGAGCCAAAGACTAGGGC
WI-18425	81	A	C	CACCCTGTCCT AGACAGATTC A	CCTCCTGTGT TGTGTGCA	AGCTGATCAGCTGTCGTTACTGTGTTTATGTGTGGCCCAGGGAAGCAAAAGATCAGACACCCTGTCCTAGACAGATTCA[A/C]TGCACACAACAACAGGAGGTGGGGGTCACGGGGCGGGAGAGCCAAAGACTAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT A	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACTATAAAAAGGAAGAAGAGAAGTAATCAAGGGAGGCCAAAGTGGGAAGCTGTATTGCTGATCTAACGTGCTGTTCCAGTTCCTCTTTTGGCTCTAAGTGGGACTA[C/T]TCTGGATACAGTCAGGGGAG
WI-18457	120	T	C	...	...	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGCTGCCCCAAGACACATTATTTTATTCTTAAATGTCCAATATCTGCCTGATGTCTGTGTTGTGCACATTGGGCACCACAG[T/C]AAATAGGCTAAAAGGCAGTCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTTGTGTACACCACAATGGCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAATATTACCATACATCCCCTCACAGCACAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GGTGCGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGGGCTGGTGGGGGGCTGAGG[C/T]GGTCACTCCCATCGTGCCCCTCGCCCTCCACTCACCCACACCTGCCCAGTCCAGTTCACGTTGAGGT

Marker	Pos	Allele 1	Allele 2	Flanking	Sequence
WI-18491	109	G	A	AACAAATGGTAGGTGGTATTAATACTATT	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAAACACAGTAAGTAACCAACAAATGGTAGGTGGTATTAATACTATTATTAAATCCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA
EST50757b	79	C	T	AGGCTCGAGGCTGCTTCT / CGTGTGCATTTCTTGTAATCCCGT / ACCCTTCACCCGCCC	AGCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGGCTGCTTCTTTTATAT GTGCAGGGCC[C/T]GGGCGGGTGAAGGGTCAGAGA
WI-17675	103	T	C	GGACATTTGGATGGTGACTGTT / GGGGAACCACCCAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTTCGTTTAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[T/C]CCTGGGTGGTTCCCCATAGATTCACCAT TGCCTCTAATGGTGTCTA
WI-16543	67	G	T	AGATAAACTACATTTGGGTTTCG / GATTCATCATTACAGGGGACTT	GATCCATTACCTAGGGTAAAATTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG G/TAAGTCCCTGTAATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C	G	GCCAAAAAGGTTGGGGGAA / TTACTTTGTACCGACCAGCA	ATCTGAGATGGAAGAGTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCCGGTGCCAAAAGGTTGGGGAA[C/G]TGCTGGTCGGTACAAAAGTAATT G
WI-17690b	79	A	G		ACAAACATGTGAAAGAAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTTGATTT GGCTTCCCTA[T/A/G]GATTCAGGAGACCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G	A	AGGCATTTTTCTAGCTGTGTTT / GGTCCTGAATC	ACAACATGTGAAAGAAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTT[G/A]A TTTGGCTTCCCTATAGATTCAGGAGACCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717b	128	C	T	GCGGAAGACAGTGAGCTGTT / TTGAGGCAATAATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATTC[C/T]TGAAGTGGAAACCACCCTCCGACCC CTGGATTATTGCCTCAAA
EST51717a	39	C	T		GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATTC[C/T]TGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CAATGGCAACATCACCCACTACCTGGTTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C	T	TGGTCACTTTGGGGCGCC / GGCTCTGCCCACGCC	TTTCCAGGTTGACAGGTTTATTCCACCCCCTTCCATCCCCATGGCCACCCCCAGGCAGGAGGAGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCGCC[C/T]GGCGTGGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A		TGTTGAAAGCAGTCACAATGTAC / CATCTGGATATCTTGTCACATTT	AAACTGCAAATAACAAACAAAACAGAAGTCCAAGAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAGATATCCAGATGTTAA
EST53389	74	A	G, C	GGAGACCTGCAGAACTTAAACAATAAATGCTC / GCCCTTTCTAAC	TTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCCAGCGAGAGCCAGCCAGGAGACTGCGAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAAGGGGAGATGGCC

EST	Pos				Sequence
EST53477	61	T	C	...	TTTGAGAGGTTGTGCAAAACTACTGTATTACAAAAATGGCACAAAAGTGAATTCAACAGTT[T/C]AATGCACATGCATACTTCACATCTTCATTCAACAACAAAGGTATTCTAACTCTACAGAACTGAATATTAGCTTCAACGGCAGCTGTT
EST64622	91	T	C	CGAGATTTTCT TCTTTATTTA TATTTTCA	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTAAACTCCCGAGATTTTCTTCTTTATTTATATTTTCATTTTCATTTTTCT[T/C]TACTGAAGCCATTTTCTTTGGTTAACTTAGA
EST67268 a	77	C	C	TGTGTATAGCA CATACTTCAGG C	CTCATCTTATTAAATGCATCGTGTGTGTGTGTGTGTGTGTATAGCACATACTTCAGGCTTCAGGC[C/T]TTGCGGCACCACCCATAGAGATGGTGAGGAAGTAACTTCTGCTTCTCATTGAAACTGTAGATCCATCGGGGA
EST78503 a	26	C	T	ACGACGCCGG CGAGT GCATTTCCGCG GCAC	GAAATGCAGAAACGACGCCGCGAGTT[C/T]GTGGACCTGTACGTGCCGCGGAAATGCTCCGTTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGATGAA
EST80253	92	G	C	...	ATGCACTTATTGGCTCCCAGGGAGTGGGATGCAGGATCAGAGTCGAGATGGGACACGCGCAGGGGGGCTGGTGTGGGGGAGCAAAGCGCCGGGGCCTGCCCGG[G/C]CGGACCCTGGTTCCCTGAGGACCAACGTGAATGGGGGCCCCACTGCGAAAGATGCTTG
EST91254	73	T	G	...	TATTCTGTAGGGAGAATAAACCATGCTTGCTTATGGGACTATCCATGGATAACTTGGTTTTTTGTTGTTGTT[T/G]TTTTAATTATAAGAATAATATGTGCTCATCATCAATGCCTTTCTCAGTAGAGCCCCAGACCTGG
EST91332 a	100	T	A	...	TCCAAACTGAAAGGAGGGGGTGGGGAAAACAAACGCATCATCATATGTAAAGCACTGAGTCCAGCCTGGCTC TTAGTAAGCATTTAATCACCTTCAAAAATTAA[T/A]TAGTGACTTACGGAAACAGGTCACTGAATAT TATT
EST91495 b	58	T	C	...	CTGACTCAAAAGACACTCCTGAAAGCAGGTCCATCCTGAGAAGCAGCTTGTATTACTT[T/C]ACAAG TCAGAACCTGTTATTAAAGACGGCAGACTGGCATTTAAATCAGCGCTGTGTCACACCCATCCTGGGTCTTT GTTCTGGCTCCTATGGTG
EST91921	114	A	G	...	CTGGCTGAGGGATCTCAAAGACATTCCACCACCACATTGAATCTTAGGCTGGAGGACATTTCGTATTCTT CAGTCAGGAATAGCACACTTCCTTTCATGAATAGCAGCTTTTAGG[A/G]TTATATCATGAGGTACA AATAAAGAGGCCCTCACC
EST92026 a	56	A	G	...	ATAGCCAAGATTTGGAAGCAACCCGTGACCATCAACAGATGACTGGATAAATAAAA[T/C]GTGGTA CATGTACACTATGGAGTACTATTCAGCCATGATCTTGTCATTAGCAACAACATGG ATGGAACTTGGGAACACTGT
EST92040 b	38	C	T	...	TTTCCATGAGGAATAAATTTGTGTTTATATAAAACCTG[C/T]AGATGAATATTTTTTTAACAGCATG ATTCACAAATGCCAAAAACAATGCAAATGCCCTTCAACACATGAATGGATTAACAGACCGTGATAC ATGA
EST98276 c	69	T	C	...	GAGTCTTGCTATGTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTAAGCCTCC [T/C]AAAGTGCCAGGATTATAGGTGTGAGTCACA

Name	No.						Sequence
EST98276 b							GAGTCTTGCTATGTTTCCCAGGATGGTCCTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTA[A/C]AGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 a	61	A	C	...	...	AACCAGGAGCT CAAGACCA	GAGTCTTGCTATGTTTCCCAGG[A/C]TGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTAAGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	22	A	C				GCCTCCAGCTGCATGACTCCTAAGCCATCATTTCGAAGATTTGGCTAATTTG[A/T]TAGTCTTACAA AGGCAGTCTAGTTCACCAGGCAAGAAGGGGTTTGTGTTGGGAAAGCGCTGCTATCTTTGTTTCAAAC TGTAAAGCAAGTTCCTC
	53	A	T	...	...		AGAGGATAGAATACATGGAAACGCAAATGAGTATTTCGGGAGCATGAAGACCCTGGAGTTCAAAAAA CTCTTGATATGACCTGTTATTACCATTAGCATTCTGTGTTTTGACATCAGCATTAGTCACTTTGAAATG TAAC[G/A]AATGGTACTACAACCAATTCCAAGTTTAATTTTAACACCATGGCACCTTTGCACAT AACATGCTTTAG
J02931	138	G	A	CAGCATTAGTC ACTTTGAAAT GTAA	TTTGGAATTGGT TGTAGTACCAT T		GGATCCAAAACACGGCTGGGTTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCATG AGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAGTGCTCTAAAAATTAAATATTTGACTTT AAGGGTCCTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGTATAATCAGTAGTGTTTACAA GATCCAAACAGTGCACTCA
L41680	88	G	A	GAGAAATCGA CTACCAGCTG A	TTTAGAGCACT TTGCAGGTATT T		CTTTTCTGTCACCAAATTTGTACCTCTAAGTACACATATGTAGATATTGTTTTCTGTAAATAACCTATTT TTTTTCTCTATTCTCT[C/G]CAATTTGTTTAAAGAATAAAGTCCAAGTCTGATCTGGTCTAGTTAAC CTAGAAGTAGTATTTTGTCTCTTAGAAAATACTTGTGATTTTTATAATACAAAGGGTCTTGACTCTAAAT GCAGTTT
M15796a	84	C	G	CAAATTTGTA CCTCTAAGTAC ATATGTAGA	TTGGACTTTAT TCTTTAAACAA ATTG		AGAGCCACCCTGTGGAAACACTACACATCTGCAAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTC ATTGGATTAATTATGTGAGTTCTTTGTCTTTAGAGTTGTTCATTGTTTG TGATTGCATGTTCCTTCAACTGTGTCCCTGGCATTCAGAGAGGAAAGCCCTCTGCTGCCATGGT[T/C]GT
M20472	103	C	T	GTTGAGTTCTT TTGGACCAAA C	ACAATGAACA ACTCTAAAGAC AAAAA		CCCTCTGACCTGCAGGCCAAGAGCAGCAGGCAGGAGTTGGGGAAAGCCCTCTGCTGCCATGGT[T/C]GT GTCCCCTCTCGGGAAAGGCTGGGCATGGGACGTTCGGGGCTGGGGCAAGTCCCTGGACTCTCTGT G
M32315b	129	T	C	GCCTCTGCTGC CATGG	GCCTTCCGAGA GGGACAC		TTCCCAGGAGCAGCAAAGGGGCCTGCTGGTTACAGCTCGGTGGAGGTGTGTATATACA CACACACACGTGTATATACACATATATGTGTATGTATATATATATATGCTTTT[C/T]C AATAACCACCTAAATTTAACAAAGGTTCCTTCAAGTGGTAGAACTTGGGGTGTATTTTACCTTC CTTCT
M33875a	131	C	T	GGTTACAGCTG GAGGTGTGT	ACCTTTGTTAA AATTTAGGTGG TTAT		TGTCTTTTTTGTAGAGATGAGGTTTCT[A/G]TGTTGGCCAGGATGGTCTCGAACTCCTGACCTCAAG GTGATCCGTGCCTGCCTCGGCCTCCCAAAAGTGCTGGGATTATAG
TIGR-A003M18 a	29	A	G	CT	TTTTTGTAGAG ATGAGGTTTC	GGCAGACGGAT CACTTGA	

Clone	No.						Sequence
TIGR-A003P30	117	C	G	---	---	---	ACAAGTTCAAAAGGAGAACTTCCTTTGTTTAATGCAGCTGTGCTCAGAAGCCTGTGTCTGATTTCCTAGGAAACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTAAAGCAGTTGTCA[C/G]ACTGGCTGCCTGAAGGTACCCTTGGAGATACT
TIGR-A004S34	156	C	T	CCAAACCTCCT	TGTAAACAGCT CATTCCTATAAA	AACTGTTTTTG A	GCTTGTCTTTATGTTAGGTTCGGGGGAAGGAGGGGGCTGACAACCGCAGACATCTGGACACCAGCAAGGGTCCAGGGAGGTTGCAGAACTTCTTTGTCCTTGGCTAACAGTCTGTGTCATGTGACAATAGCCAAACCTCCTCATTCCTATAAA[C/T]CTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTTTACATG
TIGR-A004T44b	97	A	C	---	---	---	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGAGTATGATAAAGAAGAATTTTGCATGGCGATT[A/C]AAATAGAAAACCTATAAATGTAGAAAAAGCAGGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004T44a	69	G	A	GGAAGATAAA CCAAAAATGAT	TGA	---	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGA[G/A]ATGATAAAGAAATTTGCATGGCGATTAAAATAGAAAACCTATAAATGTAGAAAAAGCAGGTCTGGACTTAGCAAAGAAACAATATAG
TIGR-A004V08	60	T	C	CAGGAAAACA GGCATTCTCTT	TCCTTCCCACA AAAGGC	---	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCTCTTA[T/C]GCCTTTTGTGGGAAGGATCAATTGGGTGCATGCACCTTAGGGGCAGTAGCTGTCAAATTTCAAAAGTAGCTGTCAAATTTCAAA
TIGR-A004V26	125	A	G	---	---	---	TCTAGCTATAAGACCAGAGTTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGACTGATTACAAAAATGTTAACAGCTGGATAAAACGGTAAAATATGCATTATCTTCACATGA[A/G]AGGTTTCAGTTTATAAATGCTAAATACTGTATTGCTTAAATACTGTATCTATTGG
TIGR-A004V28a	29	A	G	TGTTGTGGGGTG CGGATCTC	CGGAGGTTGCA GTGAGC	---	CCAGGCTATATATGTTGTGGGGTGCCGATCTC[A/G]GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCGCACCGCACCTAACTAATTTTG TATTTTTAGTAGACAGCATTGTATTTTTAGTAGAGACAGG
TIGR-A004X20	25	T	C	AAGTTTTCCTT CTCTTCTGTAG GA	TTTTATAGTTG ACTGTAACATG GAGAC	---	TAAGTTTTCCTTCTCTTCTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGTTCACTCTGGGCTTCGGCTTCATTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATCATCATGTCCTT
TIGR-A004X30	26	T	C	TTTGAAAATCTT AGAGTAGAAC CCAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	---	TTTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTTGTAATAAAATTAAAATAGTTTTAAACACTTCCATAAAGAATTAGGGGGTGCCCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCATGTTAGGGGATAAAGATATCCAT
TIGR-A004Z04	102	T	G	TTCATTTGGGT ATGCAAAACT	AAATTTCATGA AAGCAA	---	CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATGGGGTCCACAGTACCTTCATTGGGTATGCAAAACT[T/G]TTGCTTCATGAAATTTCTAATTATAAGGACTGTTGCTTCTTCTCCATATTCAATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACTGTCTTTAGTGATTTAAGACTG

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TIGR-A004Z19	85	C	T	GAGAACAACT	GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGAGAACAACTGC AGCATTTTTCTTTTTC[C/T]CTTCCCGATGACCATCTTTGGGCTGGCGGGCCAGGCCCTGGGGTGTC TCCCATATCGCTGTCTT
TIGR-A004Z42c	89	C	T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC		GTCTTAGCAGAGGAGATAAACTTTGAGGACAGCCCCAAGGCGCCAGGTAGCCTTCAGGGCGCGGGCA GGGTTGGGGGAGGTAGGAGACT[C/T]GGACCGGCGACCCTGGCTCCAGCTTCATCATCGTGTCTCTT CATCATCTGTCTTC
TIGR-A005D17c	81	T	C	...	...		TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC[T/C]GTCTAGATTCTTCTTGGCCTCTCGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D17b	79	G	C	GGGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC		TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]GTCTAGATTCTTCTTGGCCTCTCGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D44	97	G	T	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA		CATCAGTAACATATACACAATTGGTCATCAACTGAACTTTGCCTCCAATATATTCTATACAATACTT AACATTATTGAACTTAAAACTGTTACACT[G/T]TTTTGTTGGCTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR-A005E31b	27	G	A	...	...		GGAGTTCAAATTTATAACCAGCCTCT[G/A]CTCACAGCTGTACTGGCTGCTAGGCAAAGCTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTTCTTTGCCTGCTTGCCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTCTCATACCAATAAG
TIGR-A005E39	182	G	C	...	...		CTCAGTGTAAAAACTTTGTTTAGGGAGAAAAAAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGCTGAGACAGAGAATGACCCCCTGGCCTCCTTTATTTGTTCTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGGATGTCTTCTTATTG[G/C]GGATGTCTCTATTTT
TIGR-A005E42a	42	A	G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG		GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAG[A/G]CTCAATTCCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAATAAATGGTATAAGGCAGAAAATAAATAG
TIGR-A005E46	76	A	G	CACCTGACTCG GTGCTTTAC	CCCTGCCTGTG AGGTAATGT		ATGACAATGATGATAGTATTAGCCTACCGTTTGCTAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC[A/G]TACATTACCTCACAGCCAGGTTGGCAAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24	C	T	A	GCAGGGGTGA CGTATGTAGA CCTAAGC	GGGGGAGGACAC	AGAGCAGGGGTGACGTATGTAGAAC[C/T]GCTTAGGGTGTCCTCCCAGAGACGAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCCTGCTTCACGGACCTCCCCAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTCCCCCAAGAGCCGCCATATGAATCTGCCC

ID	Pos.	Alleles		Seq. fragment	Sequence
X57830	106	G	C	CT	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTCACCTATCTGGAAAAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAACCAAGGATCATATCT[G/C]TATGCCTCATTTATTCTGTCAAT GAAAAGCGGGGTTCAATGCTACAAAATGTTCTGACAGCATTTCAGCTGTGAG CTTTC
		AGTGGAACCA ACGATCATAT	CATTGACAGAA TAAAATGAGGC A		
X74070b	72	T	G	TGGATC	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAGAAATTTTGTTTATG GATC[T/G]GATAAAAATCTAGATCTCTAATATTTTTAAGCCCAAGCCCTTGGACACTGCAGCTCTTT CAGTTTTGCTTATACACAATTCATTCTTTGCAGCTCAATTAAGCCGAAGAAGCCAAGATCAAGTTT GAA
		CTTTTAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATT		
Z48804	44	C	T	...	ACTGCCGAAGTGTAGCGGCCCCAAACCTTGCTCTCATCACCAG[C/T]TAGAGCTTCTTCCCGAAGGGG CCTTTAGGATAGGAGAAAAGGGTTCATGCACACACGTGTGAGAATGGAAGAGCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAGG TCCA
D28513b	133	A	G	...	ATGACCAAAGCCACCACATTTAGAACTTGGCTGCCTTTGGAAGTCCAAGAGCTGAGCTCTCCAGCTCTCC CGCCCCCAGAGGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTGATTGACTGCATGAATGC[A/ G][TGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A	G	...	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTCCACCCTCCTGCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCAAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A	G	...	CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCTCCAACTGATCCTCCACCCTCCTGCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCAAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
					CTCCCTGCCTCCTTCCTGCCTGTGATGCTCGGTCTCAAGGTTC[G/A]CTTTCCTTCTTTGGCTTCCTCTTATTCTTCCACAAACCATTCTCAATAAA GAGGGGGCGTTTC[G/A]CTTTCCTTCTTTGGCTTCCTCTTATTCTTCCACAAACCATTCTCAATAAA GCCAAAAATCTTTCTTTCTTCTCCCCCTCCAGGCCACCTCCTGTCCTGCTGCTTGTGCTGGCTTTT
D31762	82	G	A	...	CTGGA
D37931	64	T	C	...	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTTCCTACTCTTTTCTCTATATAACTCATTCTATTAAATACATT GCACCAAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGCTTTTCTGTAAATAAGCTTCC TTT

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D63807	101	C	T	CAGGCCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTTCTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGGGAGTGTATTTTCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCGTTCCTCCCGGCCTTCTGCTGGGAGGGTGACCTGTCCCAGATGAC
D90145	21	T	C	TGGGAACATGCGTGTGACCTC[T/C]CAGCTCACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGGACTCTTCTTAACTTAATTTAATTTATTATACTATTTAGTTTTTATAATTTATTTTTGAT TTCACAGTGTGTTTGTGATTGTTTGCTCTGAGAGTTCCCCGTGTCCCGTCCCACCTTCCCTCACAGTGTG TCTGGGTG
EST14035 1a	59	T	C	ATTATCACTCTCAAAAATTTGGTGTGTGTTAAGTACTTTCTTATTTATGAGCCCC[T/C]GAGGA CCAGACATGTTATTATCAAGCCCCTTATATACCCATCTAAT
EST16668 5	71	C	T	GCATTTAAAATTCACATTGAATCATTATTTACTATTTATGATGTTACATAACAATTCAGTATCATT ATG[C/T]TTGTAGATTTCAGATGTAGGTCGTCAATACTGAGCACTTATCT
EST16904 7	57	C	T	ACAGACTATCGCCAACTTATAATGCTTAAACTTATGGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTAACAT
EST21863 9	49	A	G	TTTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACTGATACACC[A/G]GTTACTACTTACTC TTCACTCTTCAAACTGATTCCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	G	A	GGCTGTGTAAGTAGTAGAATCAAAGGTTAAGAACACATTTTATGCACTTATTCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA[G/A]TGTGACAGTGAGCAAAAAACACA
EST22623 8a	26	A	G	ATTTTAGTGCAAATGACAAAGCCCAA[A/G]AGAACAGAGGATCAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTAACACAAGTATGGGAGT
EST22644 2	98	A	G	AAAATGATTGAATTCAGCAAGTACAAGTTTATGATCTATCTACATTGTTAAAACAGCACTAAAAATAA AATTTTTAAAATGATTATCCATTATTTACAG[A/G]AAATGTGGAAAAGATGGCTTTTAAACCC
EST23587 1	31	T	A	CCTCATTTATTTAAAAAGACGGACATAAAAA[T/A]TATACAACAAACAAAACCCAAGTCACATTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106	T	C	AAAGATCTGGCATTATTCACATCATTCTAAATATTTTGTAATTACTTTTCCATGAGTATTTTTCA TGTCCAAGCATTTTAACTATCATTCATTTAGCGTAAAATACC[T/C]GAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAATT
EST24308 3	45	A	G	TAGTTTAATTTTCTGAACCTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACACATGAAAATATAAACCTCGTTC
EST24435 6	73	G	A	CTTGAACTTCTGGTCTCTCAAGTGGTCACATTTCTTTATCCGATCTTGTTGATGGACATTCAGGTTGTTTC CAGCC[G/A]TGCCTGACCCACATTTCTTTATCCGATCTTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T	C	TATTGTTGCATTATCAAAATGGTTA[T/C]AGTTTCAATTAAAAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTCCAATCGTTAGTTAATGCTCAATT

EST					Sequence
EST254769	33	G	A	:	AATGATCTTATTTTTCAGAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCCTAAAAAACCAAACACA AGAGGTCCTCTTGCTGCCTTTCCATGGACTGTGGCGGCCTTGGGCGGTCTGCTGA
EST261832	70	T	A	:	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG AT[T/A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST272311a	28	T	C	:	AGAAAATAAGGTGCTACCAGAACTCATGT[T/C]GATAGCGGCTTTCTTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACAGACTGTGCCTCTAACAACACGGTGACTCTGA
EST278165a	26	T	C	:	CAACTCAAGGTACAAGACAATTGCAT[T/C]TAACATTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAGGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST285880	78	A	T	:	GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAAATCA[A/T]GGTAGAAGGCAAAAGAGAAGGAGGCAGCCATCTCTTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGGGAT
EST302265	25	A	C	:	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGGAATATAAACTACTGAACAAGACGACTTGTCTAACTTAAACAAGACAGACTCATTTCCTTGA G
EST309359a	59	C	G	:	AGCTATGGTAGAGCAACAAATTCCAGTGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST325157	25	G	A	:	CCGAATATAAGGAGAAAAAATGGTGGC[G/A]TGCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCCTATGAATACTGGCACTGTTTATTCATGTTTATTGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST332744	27	T	C	:	TGCTTTGTTTCCCTCCAAATCCTAAAA[T/C]GTGTGTCTTCAAAGAAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST333527b	75	C	G	:	TACACATTATTCAAGAGAGACCACCTGACATGCCATCTCCTCCGCAGAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAATATCTTGGTGTCATATCTAGGGG
EST334241	126	A	C	:	ATTTTCCCACAGCAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAGAAGTGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST334887	90	A	G	:	CCTTTGGGGGAGTTTAAGCCAGCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST335081b	45	C	T	:	AAAAAACATGCTATTTGAACAAACTTTTTATAAAGAAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

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EST33508 1a	36	A	G	---	AAAAACATGCTATTTGAACACAAACTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77	C	T	---	ACAACATAGGACTGGTTATTCTTGGTTTGAAAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]TCTTTGAACTACAGCCTGAATCCCCC
EST34739 3	97	T	A	---	GAAGTATCCTTCCCAGTGGCAGGAACTGAAGACTCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A]GGTGCCTTACAACTCCAACTACTGCAGAATTCT TGTTGTGCCTCATAAACA
EST34792 6b	104	A	G	---	ACCTGACTGCTCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCTTAGTCCTATTACA AAGATTTTGTTGCTGTG
EST34835 9b	93	T	G	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGTGCTTTCTGG[T/G]GGGCCTTAAAAGAAACAGACAAATTGTGCTAAAGAT
EST34835 9a	82	G	A	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAAGAAACAGACAAATTGTGCTAAAGAT
EST35230 0	93	G	T	---	CACAAAGGTCCACTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33	C	T	---	TCTTTTCAAATTTTTTGATGTAGGCATTTAATG[C/T]TATAAATTTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTGTTCCATTTACTTAGTTCAGAACTTTTCAATTTCATCT
EST35708 9	32	C	T	---	CTGCCCCAAATTAACTTTTAGGCAAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAG ACAGCTTAGTATATGTTCATATGCAGCGTGTTGCTTCCCTCTCTGAGGTTGGCACCTTCCTGTTGTG ATGTGTCAAAGTGTGGCT
EST35747 9	51	C	G	---	ATCCAGTGCAGAGTTGTGAGCTGGAGACATATTTCAACCACAAAGGCTCCA[C/G]ATGTTAAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCTTCCAGTAGGGTTGGAGATT G
EST35751 9	89	C	A	---	TGGTCCATTATTATTAAAAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCATGAAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGAACAATAAGAAAGCCAGGT ATATAATTAAGGCCCTGTGA
EST36301 4	93	C	T	---	CACCTGTTCATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGCCTACAGC AGTCAGGAGGCAGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33	G	T	---	GCCATCAGCCCACCAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGCACCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTTCTCGT CACAGGGGGTCTTAGTCGT

EST36620 6	50	G A	---	GACTTTATTAGATAAAGGGGTTTCGGCTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89	C G	---	CCTGTGATGTGCATGGGTGCCTGAGCAGTCAGTAGCAGTGGCTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCCTA[C/G]AGGGGACATATCCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62	C T	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACTTTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103	A T	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAAAACTACCATGCCAGATCTCCACCCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCCTAAGCTCATCATGAG TTAA
EST36987 4	126	C G	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCCACAGGACCTGTAAATATT TAAATAATAATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88	T C	---	GGTCTCACTCTCTTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105	T G	---	AATAGTCTATGGCTACGGCCCCGTGGGATGTTAAAAATTGGGATTTAAATTAAGATTGTGAACATG CAAACCCAGCAAATTTCTCAGCTTATATTTGAAAGTC[T/G]GCAGGAGAAAAAATGGGGTCC
EST37284 2	93	G T	---	AAAAGACCTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAACCCTGAGATAGCAACCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90	A G	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACTAAAGATATCCTCCTGCCTCAGCCTCCCAGGTAGT TGGAACTATAGTAGGAGTATCTTA[A/G]CCCTGCCCCTGCTAGAACTTCAAGTTTTGATGGGCAAATCCA CCCCAGGAGGACAGGACAA
EST37374 1	45	C T	---	CCTGCCATGATAATGTTAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101	G C	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGTTGAGCGGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGTCCTGCA[G/C]GTGTCCTGGCAAGTTGCTGACTTCTCTG TGTCCAGG
EST37376 8a	41	T C	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[T/C]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGTCCTGCAGGTGTCCTGGCAAGTTGCTGACTTCTCTGT GTCCAGG

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EST373789	63	T	G	ACACACAAAAAAATGGTGGCAGAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAC[T/G]AACATGCCTCAAAAAGAGAGGGGAAAAACTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST374524	46	G	A	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTAAAACACCCTAAATCAATGACGTAGAA
EST376136	34	A	G	CTAGGCATGGGCTTTACAGTCATTATTTACC[A/G]GTCATGAATTCATTAAAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCTCCCAAATCACCCTGCGTTCATGGATCTTCCATTCTAA
EST380254	56	T	G	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTACATGTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EST380686	57	C	T	TCTACCAGGTCACCAAGTATCTGTATATGCTTAAGTGGCATTTCATGTCACTTA[C/T]CGCATGG AAGAACGCTCTCCTTTAATTCCCTAACTCTCTTCTGGGAAGACAGAACGTGCACAA
EST384206a	100	T	C	TAAATCAAGGCCTCTTTCATTACCAAAACAAAACAAAAAAAGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACTACGAC[T/C]GTCCCTGCCAGTGCCCATGGGTCCGTGCCT TATTCATTCTCTCTCTCA
EST389505	25	T	C	TTTATTTGCAAAAGTAAGCAGCCGGT[T/C]GTGGTCCCTGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGTGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST390536	90	T	C	TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGGTTAATATATCATTTTATTGGGATGAGATCA TAGTCTTACACAAATGCTATGT[C/A]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST393311	70	G	C	TCCTTCTTGCTCTCTCTAGCACTCAGACCACCAAAAGAGAAGCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST405447	31	C	A	GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACTAGAAACTCTATTGTACTTCT CACTTATCACATTAGCTATCGCGAAGTTGAAATTT
EST405484	37	T	C	TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC[T/C]TCAAAATAACTAACTAAAATCTGTA AGATAAAATGCTGGAATTTGAGAGAGGCACATGCCCTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTC AATAATCTGTGGGACTCA
EST405491	42	A	G	TGTTTCTCTAGAGAACCCTGTGTGTGATACATACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCACTTGAACCTGCCCTGCCAAAGCACCTCTA CCCTGCACTTTTGGGGAG
EST405791	81	A	C	TGTGAATTACACATCAGTAAGGCAGTTACAGAATTTCATTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGATTAAATACGAACAAGGTCTTCCAGGAAG
EST405843	68	A	G	TTGTATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGACTCCCACAATATCCTATGTTTTAAGCT

ID	Pos			Sequence
EST51340	51	G	A	GATCAAACTGTATTGCCCAGGCCAGCTCCTGAAGAACTATGTGAACTATGAAC[G/A]TCTCAGCCTAGAAGGATAAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCAAGCTAGATAGGCCAAGGATTATT
J04162	134	T	C	CATGGGAGTAATAAGAGCAGTGGCAGCAGCAGAGGCGCAGCATCTCTGAACATTTCTGTGGATTTGCAACCCCATCATCCTCAGGCCTCTCACAAGCAGCAGAGAAACATAGAACTCAGAGCACCAGATCCTTATCCAACTCTCGA[T/C]TTTTCCTTGGTCTCCAGTGGAAGGGAAAAGCCCAGTGAGTAGCTG
K01506	63	T	C	CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTTCTTCTCCACTTCATGTGAAAACTAC[T/C]CCAGTGCTGCTGACTGAATTGCTGACCCTTCAGCTCTGTCCTTATCCATTACCTCAAAGCAGTCATTCCTTAGTAAAGTTTCCAACAAATAGAAATTAATGACACTTGGTAGCACTAATATGGAGATTATCCTTTCATTGAGCCTTTATCCT
L18877	69	T	C	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCCAGTGCACCTTCCAAGGCCC[T/C]ATCCATTAGTTTCCCACTGCCTCGTGTGACATGAGGCCCATTCTTCACTCTTTGAAGAGAGCAGTCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTCCTGTTGGAATTGTTCAAATGTT
L31848	36	T	C	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTTGTCCTGGACCCTGTAGGGTGCCATTTTGGAGTTCACAGCCTAGAGAAGAAAAGGCTTTGGGCCTGGTGGTGGCCTGCATAGGCCTGTAATCGTAGCGCTTTGAGAGGGCTGAGCTGGGGGACTGGCGT
L38517	137	G	C	GGGTCCAGAAGCCCTCTCAGCCAGGAGGAGGCTGGCCCTGGAAGGGAGGGACCTGAGCTGGGGGACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACCACCATTGAGACTTGACTGGCCAACACCAGCGTCCCCCACCC[G/C]CGTGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCTCTCCTAGAGACCTTGAG
L39059	123	T	G	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCAAGCAATTTGGAGCCAAGTTGAAGGGACCAGGGCACCAAACAAATACAGTAGTTTCTTTGTATATT[T/G]CGCCTGAAGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGCCCGGTGGGCCCTGTGTTGCTGTGTCTGTGG
L41268d	173	G	A	CAAAGTTGTCTCCTGCGCCCATGAGCACCACAGTCAGCCTTGAGGGGATCTTCTAGGGAGACAACAGCCCTGTCTCAAAATGGGTTGCCAGCTCAATGTACCGACCTCCAATCTGAAGGCGTGAGTCTGCATCTTAGGGCATCGCTCTTCCCTGCTCTTCCCTCCTCCACCACAAATCTGAAC[G/A]TGCCTCTCCTTGCCTTACAAATGTCTAAGGT

L48728b	111	T	C	AAGTGAACAGAAAGCAAAGATGGATTGTGTTCCTATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGAGCTCAAGTTTTTGGTTTACTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G	A	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCCTTTTATAAACATTGGTATATTCCATTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T	C	TAGGGATCTGTGCCAGGCCATTCGCACCACCACCCCACCCCCTGTAGTGCTCCCACCCC TGGACTGGTGGCCCCCACCCTGCGGGAGGCCTCCCCATGTGCCTG[T/C]GCCAAGAGACAGAACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCCAGGGGCGCTCCGCCCTCCCTTCCTTCTCGCTTCTAATA GC
M21539	114	T	G	TCACCTGCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCCATGATGATCCCGACAGCAAAAT[T/G]TTTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT TCTCTTTGGGGTGC
M26041c	173	A	G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCTCCAAATGTTCTCCTCTCACCTCT TCTGTGGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGACTTC CTGATTTTTTCTTTTCTTTCTCAAGTGTTACCTACTAAG[A/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A	G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCTCCAAATGTTCTCCTCTCACCTCT TCTGTGGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGACTTC CTGATTTTTTCTTTTCTTTCTCA[A/G]GTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C	G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCTTC[C/G]CAAATGTTCTCCTCTCACC TCTTCTGTGGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTTCCCTGAC TTCCTGATTTTTTCTTTTCTTTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G	C	TAAGGCAGCTGTCAGGGAGGAGGCCCAGTCAGCAATTCCACAACCACCCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCTTCTTGTTCCAAATTAACTCTTAGAAGAAACCCCA CAAATAAAGCAATTCAATC
M81695	34	G	A	ACTTACTTACCCTCACCTGTCAGGCTGACGGGGA[G/A]GAACCACTGCACCACGAGAGAGGCTGGG ATGGGCCTGCTTCCTGTCTTGGGAGAAAGGTCTGCTTGCTGGGAGGGGCCCTTGTCTGTTGTCAAGGTTC CAACTGGAAACCCTTAGGACACAGGGTCCCTGCTGTGTTCCCCAAAGGTCTGTGCTGACTTGACTTGCAATTCTACC T

ID	Position				Sequence
U06641d	166	C	T	---	CTCCTCCTTTATTTCAGCATGGAGGGTTTAAATGGAGGATCTCCTTTCCTGTGACAAAACATCTTTCACAACTTACCTTGTTAAGACAATTTAAAAAGATCTTTCACAACTTACCTTGTTAAGACAAAATTTATTTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTTAAGCTATGAAAATACAATGGGGGA
U09607	39	T	C	---	GAGGCCTTATGAGGGTCCTCTACTTCAGGAACACCCCCA[T/C]GACATTGCATTGGGGGGCTCCCGTGGCCTGTAGAATAGCCTGGCCTTGCAATTGTTAAGGTTCAAGACACAGATGGGCATATGTGTCAGTGGGGCTCTGAGTGCCTGGCCCAAAGAAGCAAGGAACCAAATTTAAGACTCTCGCATCTTCCCAACCCCTTA
U09608	82	T	C	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTCGGGAAAGTCTGGTCC[T/C]ACATCTGCCCGCCCCTTCCCAGCCCCTCCTCTGTTCTTCATTCATTCAACAAAATTTGGC
U10694	20	C	G	---	GTGACATGAGGCCCATTCTT[C/G]GCTCTGTGTGTTGAAGAGAGCAATCAGTGTTCTCAGTGGCAGTGGGTGGAAGTGAGCACACTGTATGTCATCTCTGGGGTTCCTGTCTATTGGGTGATTTGGAGAATTTATCCTTGCTCCCTTTGGAATTGTTCAAATGTTCTTTAATGGTCAGTTTAATGAACTTCACCATGCAGAGTAATGAATGACAGTA
U13877b	162	T	C	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTGCTATCTTTGTGACCTTGCACAAGTTGTTAACCTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGTAAAGCACAGAGGAACAGCCAAGAGAT[T/C]TTACCGTGGTCTTACTAACATATCCTAACTTGGGGTTTACCTTCAGCA
U15555	187	T	C	---	TTTCTGTCCACTTCACCTGGTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAAAAATGCTTTGGAAGAATTAAATAAGCAAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGTTCCAGTAAAATTTATGAGTCCACGACCCCTTTCTCAAGCAGTCTGGTCCATG[T/C]GGTCTCATACCTCATATGCAGGATTCATTCA
U17077	122	T	C	---	TCCAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACTAAAACGTCCACGGATTAACAGACGTCCTTGCAGACTGAGCGATGACACCACACT[T/C]TTGTTTGGACATTTAAATTCACTCTGCTGAATAGGAGGAAGCTTTCTTTTCCTGGGAAAACAACTGTCTCTTGGAATTA
U18543	58	T	C	---	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAAACT[T/C]AGAAGCTCCATCTTTAATGTTTTAATTGTTTATTTGTTATGTCCCCCTGGCCTCCCACCTAAATTTAGAGCTTTAAAGATGCACTGCCCAAATAGGACACACGATGGTGTTGATTGATTAGCAATTGATTAGGCACTTCCAAGGCTTTAGTAGTAGAGAGAGCC

ID	Pos			Sequence
U25975b	164	C	A	TCACTGCTGTGGCCTCATACTCTCTTTTCCATTTTCTACAAGAGAGCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTG AAGACAACCAAGAGAGAAATTGCAAAAGA[C/A]AAGTATGACTTTTATATGAACCCTTCTTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C	G	TCACTGCTGTGGCCTCATACTCTCTTTTCCATTTTCTACAAGAGAGCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTG AAGACAAC[C/G]AAGAGAGAAATTGCAAAAGACAAGTATGACTTTTATATGAACCCTTCTTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A	G	CAGGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTTAAAGTAGTTCCTATTTCTATCCCCTTAAAGAAAAT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAA TCC
U28413	29	C	T	ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATATTTTTCCTCATGTTTTAAAATGAGGTT AATATTTGCATAAAATCCTAAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCTTGATCC CAGATGTTGTGGCCCTGGGAAAGCCCTCATTGCTACAGTACAACAACAAGTCGTTGTACCTCAGTT G
U30884c	89	A	G	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATCTGATGGCTTGAACTTGCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A	G	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATCTGATGGCTTGAACTTGCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A	G	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCCGTGTCATCAA[A/G]CCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G	A	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCC[G/A]TCATCAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT

ID					Sequence
U31416c	76	G	A	---	AGTTGCCAGCTCCCATGTACCAGCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATGCTCCTCCTCAC[G/A]CCACAAATGTCGGTGCCTCTCTTGCTTACAAATGTCTAGGTCCCACTGCCTGCTGGAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCCAACCTAACTGGCTTACTTCCT
U31416b	68	C	T	---	AGTTGCCAGCTCCCATGTACCAGCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATGCTC[C/T]TCCTCACGCCACGCCACAAATCTGGTGCCTCTCTTGCTTACAAATGTCTAGGTCCCACTGCCTGCTGGAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCCAACCTAACTGGCTTACTTCCT
U37519a	78	C	T	---	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCCTTATGCTCCCAACTCACATTGTTCCTCCAGACCGGCCAGG[C/T]TCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTGCCAGGGCTGCAAAGCAAGGTCTTGCTTCTATCTGGGGGACGCTGCTGCGAGAGAGGCCGAGAGGGCGCAGAACATGCCCAGGTGTCC
U37690	54	A	G	---	GACCACGCTGAAACCCACCCACCGCTGTGCTGACCATGGGCCCTGAGCGTCCT[A/G]CCCGAATTCACGAGGCTGAGGCATCCGGGAGCTGGCCGTAATGCCTGGCCGCCAGTGTGTGTATCCCATACCCCACTCTGGAAGGAAACCATCCAGTAAAGGTCTTT
V00540	39	T	C	---	TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]CACCAGTCCACACTTCTATGACTTCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTCAGATCTTTTCAGGAGTGTAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCCTTACAGATGACCATGCTGATA
X15943	106	A	T	---	TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTAAAACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAAAA[A/T]ATCCATAAGGGAAGGTACCCACACCAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAATTTGGATTCATCTGTGTTTCATGTCTCTCCTTGTAACCCTGAGATCATCAG
X52011b	148	C	T	---	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTAGGAACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAAGTTGCGAAAAATTGCGAAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTCGGGCTTTTATTTTTTGGAACTGCGAGTGGCTTAGGTCTAGCCT
X52011a	118	A	C	---	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTAGGAACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAA[A/C]GTTGCGAAAATTGCGAAATCTGTGTGCACGCTCAAATGAAAACGCCTTCGGGCTTTTATTTTTTGGAACTGCGAGTGGCTTAGGTCTAGCCT

ID	Pos			Sequence
X54741	24	A	G	CAGGGCCACCTGTCTTCTCTCTCCCCAC[A/G]TGCACAGCTTCCTGAGTCACCCCTGTCCAGCCAGCTCCTGGCACAAATGGAACTCCCCAGGGCCTCCCAGGACTGGGGCTTGCCAGGCTTGCAGGGCCTGCCCCACCTGGCCCCTTCTCCAGCAAGCAGTGC
X54869	99	A	G	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAAATAGAAATATTATGATTGCATAAATCTGAAAATGAATTATATGTTATTTGCTCT[A/G]ATACAAAAATTCTAAATCAATTATTGAAATAGGATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGTCGGGCTCATTTTGCTCAACATGGTA
X66924	147	G	A	GCCGTGTCCTGACACCTCCAGAAACGCAGGTGCTGGGCCCGTTCTGCCTGGGACCCCGGGAACCTCTCCTGCCGGAAGCGGCACGGCGCAGGGATGGGCCCCAACTTCGCCCGCTGACTTCACCAAATCCCTTCCTGGAGACT[G/A]AACCTGGTGCTCAGGAGCGAAGGACTGTGAACTTGTGGCCTGAAGAGCCAGA
X78932	62	T	G	GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATATAAGATAA[T/G]TCATACTGGAGAAAACTCCCAGAAGTGTGACAAATGTGACAAACATTTAATTAATTCTCATACCTTATTGCACAGGAAAGCATTTATACTTGAGAAATGGAAAGTCATTATATCTGCTCATATCTTAACATCAGCGAGTT
X80026	25	T	C	CTCAACCCATAACCTCAACCACATC[T/C]TATCCTCCACCCACATCCACCTCCATCCCCAACCCATCCTCATCCCCAACTACAGCCCCAAACCCAGCGCCCATCCCAAACCCACCAGGGCCATCCCAAACCCATCCCAAGCCAAAACTCAACACCATCC
X80197b	99	G	C	ACCCCAACTCAAGTCCCAGGCCCCCAGGGCGCATCTTTCCTGCCCTGCCTTGCTTGGCCATCCAGTCCAGGCGCCTGGAGCAAGTGCTCAGCTACTTCTCCT[G/C]CACTTTGAAAGACCCCTCCCCACTCCTGGCCCTCACATTTCTCTGTGTGATCCCCACTTCTGCCGCCTGCCCATCCAGTCC
X80197a	28	A	G	ACCCCAACTCAAGTCCCAGGCCCCCAGGGC[A/G]TCTTTCCTGCCCTGCCTTGAAAGACCCCTCCCCACTCCTGGCCCTCAAGGGCCTGGAGCAAGTGCTCAGCTACTTCTCCTGCCCACCAGTGGGAAAGGCCACCCTAGAAAGCATTTCTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGT
X85106	150	G	A	GGCACCCAGAGTGACCACAAGTCCAGCAGGAGGCGCGCCTCGCCGTGTCCGTGTCCTGCTGCAGCCCCGGAGAGGTCCTGACCTGGGGGCTTCTCCAAGCC[G/A]AAACCAAATGCCCCCTTCACCTGGCGCTCCCGAGGCCGGGGGCTTCTTTTCTCCCCAAGCGGGGGCTTCTTTCAGAGC
X87160	128	T	G	ACCACCAGCCATGGTCTAAGGACACATGGATGGGGTGCCCCAGAGCGTGTGCACAGGGGACCCTCTGCCCCACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCTGCTTTAAACCGCAAGATGGGCGCC[T/G]GGGGCATGCGGCAGGAGGAGCCATCCGGGTACTACGGGGTACTCCACAGCCAACTCACAACTGTCCAGGCTGAGATAAATCCCGGGA

X87344	34	C	T	CATCCCAAGGCACTGGTGGTGACTCTGCTTCCTG[C/T]ACTGACCACCAGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCAAGGGGACTCTCTGTTTCCATTCTCCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAAATCATTTACCGACTTTAGTGCTTTTTT
X87838	179	G	T	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCTATGGGAACAATTGA AGTAAACTTTTGTTCTGGTCCTTTTGGTCGAGGAGTAACAATACAAATGGATTTTGGGAGTGACTC AAGAAGTGAAGAAATGCACAAGAATGGATCACAAGATGGAATTTA[G/T]CAAACCCTAGCCTTGCTT GTTAAAATT
Z14138	81	A	G	GTTCTGCTGCCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCTCCAAGCGCCCTGTGTTTGACATGTGAAGCTATTTGAT ATGCACCAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191	A	C	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGAATCTGGGTAATTAAAAACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTGGAGATGGAGTATACATGACT GCAACTGTATTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTC CAGTACTGGTTTCCAA
Z23091	159	G	A	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGTCTTGTCTCTCCCTCCCCTCCCC CACTCCTCCTCTCTCTCTCCTTCCACTGCCACGCCCGCAACCCCTCCTCCTCTCTGTCCCCGGTCTCTGGAAA CTCTGTGTCGCTCCTTCAC[G/A]GGCCCGCAACCCCTCCTCCTCTCTGTCCCCGGTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125	G	A	GTTGGCATTGTTAGTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTGAAACCTGACCTAGTTGTGCTCCAGGACCTA[A/G]CGGTGC TCACTCTACCTTGTCTTGTGTTGGTAGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
11595	125	A	G	GTTGGCATTGTTAGTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTGAAACCTGACCTAGTTGTGCTCCAGGACCTA[A/G]CGGTGC TCACTCTACCTTGTCTTGTGTTGGTAGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
1241	131	G	T	TATATCACATTAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAA TGGTCTTGTCCTTTCAATAAAAAGAGTGACACATGATTGAACATGTGTTTAGATAAAGGGCACTT[G/T])GCAGGAGTGTTTAGGATGAAGAGAAGAAGATTAAGGAAGATCAGGAGAAGAAAAGTAGCAATGGGA ATGAAAAATAGGAGGCCCTGAGATCCCACTGGATAATCTAAAAAACCAAGAGAAAG

1282	130	C	T	GTGCGGATCACCACTACAGTCTAATTTCAGATGTTTCATTACCCCTAAAAGAAGAAATCTTGTACCCATTA GCAATTATTCCTCATTCCTGCCCTCACCCCAGGCCTACTCTTTATCGCTATAGATTGCC[C/T]ACT TGACATATCATACACATGGAGCCATACATGTGCCCTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C	T	AGTATCACACATACTTAATATATTAGATATACACAATAATAAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTAATTTACAACACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAAACCCTTTAAAAATGTCTATGAACAAGTACAA TTTCTTTTTGAGTTCTGCAGAGCAATGACCACTACTAGAAGAAATATTTTAAAGGC
6817	118	A	C	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTCTGTTCTAGTATTTGCTTTTTGTAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCTG TGTGCTCTACTGGCCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGCGCCCTGTGCAGATGGCCTTTTGGTTGGTTGTCTTAG
6819b	212	C		CCATTTTATTTTTCTCTAAAATTTAAAATAGAAGACTTTAATGGAAAACATTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTTGCTTTAGCAAA CAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCA
6819a	166	G	T	CCATTTTATTTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTGCTTTAGC AAACAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCA
681xx	39	A	G	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCACGAATGTCCTTAAGATATGCAGCAAGCACAAAATCTGTCATGGT TTAACAAAAGAAATGAAACGTCTAGG
6972b	149	G	T	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT CTGGTAGAATTTCAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGC CACAATTTCAGA[G/T]CCTGTATTGGTCTATTCGGTCTATTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A	G	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT CTGGTAGAATTTCAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTTCAGAGCCTGTATTGGTCTATTCGGTCTATTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

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7598k	210	A	C	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTTCCT CAATGCAG[A/C]
7598j	208	A	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTTCCT CAATGC[A/T]GA
7598i	192	G	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCC[G/T]TATTT CCTCAATGCAGA
7598h	144	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTT CCTCAATGCAGA
7598g	142	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTT CCTCAATGCAGA
7598f	120	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAACCAGATTTTACCTTG[A/G]GGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTT CCTCAATGCAGA
7598e	83	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGCTAA[C/T]CAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTT CCTCAATGCAGA
7598d	77	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGC[C/T]GCTAACCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTATATTTCCCGTATTT CCTCAATGCAGA

ID	pos				Sequence
7598c	56	A	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGAGACACCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A	T	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATA[A/T]CCTTGAGGTTCCT
7998b	94	A	C	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCTA[A/C]TCTCTCAAGGTCCCAAATAACCTTGAGGTTCCT
7998a	75	A	T	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATCTTCTCAAGGTCCCAAATAACCTTGAGGTTCCT ATACTTT[A/T]ATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCAAATAACCTTGAGGTTCCT
8071	119	A	G	---	AAATACAGAATTTATTTAGAAAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTCCCAATAAAATGGAATTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCATTGAACAATGGCTAGTTACTTGCATTTTTGGCATTGTAATCACTGAATC TGGGTTTCCTCTGAATTCCACACAGAGCATGCACTACACAACATTTTATCAT
8467b	93	C	T	---	AAGGCTTCCTCTCAAACATCAGTCCTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAATCCACTTGCTGTAA[C/T]GGTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70	A	G	---	AAGGCTTCCTCTAAACATCAGTCCTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTGCTGTAACGGTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84	C	T	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTAG[C/T]AATACTTCATTAAATCGAAAAGAAAAAATTGCTTTAAGGAAAAAA AACTGGCTTCAGCTAG[C/T]AATACTTCATTAAATCGAAAAGAAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTAAGAACAACAATTAACATTAGTCTTTAAAATAAAAGGAGGGCTAATGTTTCATGGTTGCT TTATACATCCTTCCTCCAATACAGAACCAGGAATGTAATTTTCCTAACTCAG

WI-18562	29	G	A	---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAGCTTCTCTTATTTCACATAGCTAGTTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATTTAGCATTAATCAGAAACGA
WI-18618	51	A	C	---	ATAGCAGACTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAAC[A/C]CGCTCAGCTTCGTTACAATGAAGAAATGGTTTCCTTCGATGCAAAGTATAATTGTAAACCACAGTGCTCGCACAGTTCAC
WI-18683	22	C	T	---	TAAGCTGTTCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGAACTGACAGGCCAGTGGGTCCACCCAAACAAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G	A	---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTGTTCTTTTACTACA[G/A]CCGGAGTGGTAAATACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAATGCCCTTCCGTTCGAGAC
WI-18563	94	A	G	---	AAATAAAGTTTTATTGGCACACAGCCAGCCACTGGATGACACATTGTCCACGGCTCTCATCTTGCAATACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T	A	---	GTCCTATTTCAATTTAGCTAGACCCATTCATTCTGTTTAATGGCTACATTTGTTTTCATTGTGAGAC[T/A]GTGCCATAATTTATTTATTCAGTGCCATATTGAAAGACATTTGGATCGTTCCCAG
WI-18723f	94	G	A	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTCTGTGTAGATTTTTGAAAGTGGTAACAGGTACATAGGTAACCAAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T	C	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTCTGTGTAGATTTTTGAAAGTGGT[T/C]AACAGGTACATAGGTAACCAAAGTATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A	G	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTCTGTGTAGATTTTTGAAAGTGGTAACAGGTACATAGGTAACCAAAGT[A/G]TAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G	A	---	TTTATTACAATATTTAGGTGGCACAATAACTAACAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCATAGACTTTGCAACTCAGCCAGAAGTAAAACTCGAAATA
WI-18715	76	G	A	---	TTATTCACAAAAGTGATATTGCAGAGGGTGTGGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTGTACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTAATAAAAAATAATGGAGCTACAACCACCCC
WI-18535	107	G	A	---	GTAAATAAAGTTTATTGGCACAGCAGGCCGAATCCAGGCTCGTTCATTCATATGCCATTGACATCTGCTGTTGCCCTACACAGCAGGGTGGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTGTTAAAGCAGTGGTCCCCAACCTTCTGTGTCCCCGTG
D17525	107	C	T	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTCAGTTCTGGGCAGGTGACTTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAAA[C/T]GCTATACCTTACCTACCTCGTAAAAGTCTGATGAGGAAAGAAAGATTAACTAACATAAGTAAGATATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTTTCAATAAATGCACCTTAGCAGAGAAGGTCGATGTGTCTACCAGGCAGACGAAG

				Sequence
DWU-133c	313	A	G	TAATTGGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAGTTTTGAATTTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCTTTAAAGATATGATTAGACT
DWU-133b	236	T	C	TAATTGGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAGTTTTGAATTTTAATAGTAA[C/T]/CTAAAGATATGATTA AATTCAGTAAATGGTATCACTCGTTTACCCTTTT/C]TAAAGATATGATTA
DWU-133a	199	C	T	TAATTGGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAGTTTTGAATTTTAATAGTAA[C/T TTCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTACCCTTTTAAAGATATGATTA
DWU-36	102	C	T	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCTTCCTCAGTGCATCTGGGAAGATTTCTACC[C/T]GACCAACAGTTCCTTCCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCCCAGCCCACAGGTGTTTATACAGCTTCAGCTTTTGTCTTTTCTGGAGGAG AAACAAATAAGACCCATAAAGGGAAAGGAATTCATGTGGAATATAAAGAT
DWU-387	169	G	T	GTGTATAAAATGCAACTGTTGATTTCCTCAACATGGCTCACAAATTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAAACTGCACTGCCCAACAAGTTCACTCATTAAAGCATTATTTTTA CTCTTTTGAGGTGAATATAATTTATTTATTACAAATG[G/T]AAAAGCTTCTTAATACTAAGTATATTTTTCA GGTCTTCACCAAGTATCAAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172			ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCCATTTAAAAATCACTGTAATTAATTAGTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCATTTGTTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAAATGTCTTTCTGTTAG GCCTTCTTCTTACAATGAAGATGAATTCTTCTAGTTTATGGTTA
DWU-447	85	A	G	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCCATTTAA[A/G]ATCACTGTAATTAATTAGTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTATTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAAATGTCTTTCTG TTAGGCCTTCTTCTTACAATGAAGATGAATTCTTCTAGTTTATGGTTA
DWU-476	63	C	G	GTAAAATTCAGTTTTTTCCAGTTCCTCTTTTGTGCTGCTTTCTCAATTAGGCGTTTAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGGAGATTTTTT

DWU-505	67	A	T	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAAATTCTATCACCATACAAAATTTA[A/T]TGCAGTATTATGTTTAAAGCACAGGTGTACCGAAAAACTGTGAAAAGTCTGAATTTATGGGTTCTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGATTAACTTTTGACTTTGAGCTTAAACTTTTAA
DWU-512	131	A	G	AAAATCCAGGCATTTCGAATCTGTTTTCATGATTATAGAGGGTTTACACAAAGTGCCACTTATTAAAGAGCTTCCACAGTGAAGATGGAGAAGGTGAACTTGCTTTGAATATTCCAGATGTGTTTGGTC[A/G]TGCGTATGGCAGTGAGCAGGTATGTGTTTGCTTGCTTCCAGAGTGAAGATGCCGAGAAACTATGAACGGGTTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTCAGCTTGTTTCTATACTGTTTGTAATATACAGTTTTGTAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACACCCAATTTAAAAAATAACATATTCTTGCTTCACAAATATAGTTGAACAAGATTTCCCTAAAAATTCCACCAGGATTAATCTCTAAAATTCTAGTCTCTGATTTGC
DWU-59	94	C	T	CATTCTTTGTGAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGGCCCTTTCTTTGTGTGAACGTCACATTGGC[C/T]GAGCCGTGTTCAGTTCCCAGGTGGCAGACTCGTTTTTGGTAGTTTGTTTGTTTAACTTCCAAGGTGGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATGCCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C	--	CTTGATCATGGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGCAGCAGGTGCCGAGGGGTCTGAGATCAGAAAAAAGGCA
WI-19856b	63	C	T	CACACTGGCATCTAGGCCTTGCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCCCTCCTGGAGAA[C/T]GCTGCGTTCCCCAGCCCCACCACCGGCTTGCACCACACAGGCTGTTGAGGCAGGAGGTGGGTAAGACGTAGCTGTAGACCCAAAGCAACCACCAGCCCTGGGACCCTGCGGGGAGGAGCACTTTAGAACATGGAAAAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACACATAATAACAAAGT
WI-18014	40	A	G	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGTGTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCTA
WI-18036b	97	T	A	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTAATTCTTCATAA[T/A]CTGACAGGTCAAGTCAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18036a	27	T	C	TTCCAATGTAAGAGTCAAGTCAAGTACCAAGTT[T/C]AAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTAATTCTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18046	72	C	T	TGTAAGGTGACTTCCTATAGCTTCCTAAACTGTCAAACTTCATTTACTGAGATTATTCAGGCCAATGTGTTC[C/T]TTGTTGGGTCTGAGATTGATTATCAGCTGGGTAAGTAACCTGTTCCTGTTTCA

ID				Sequence
WI-18063	105	G	A	AGGCTTAAACTGATAACAATTGCCTTTAATCACATACAAAAACTCTGCACTTTCATTCCTTCCTCCCATGTTTTCTGATTTGATGTAAACTTAAAATTTGTTG[G/A]TCCTTTAACAATATACTGGTCCAGTGCA
WI-18078	86	A	T	AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAACTGAGATTCAAACCTGGTCAACCTGGTCCAGTGTGTTGTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T	C	CCAAAGCTCACTCAGTATTAATCATCTGCTAATTTCATCCTTTGTTAATTCCATCAGACACTGTGGTTTCATCTCTAGAAGTTTGACT[T/C]GGGCCTTTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18091	38	T	C	GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGA[T/C]TTGTAAAATGGATTGGAGTACTTACCACTATTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAATTTGGTTCTT
WI-18142	66	T	G	TTCAAGATAATTACAAATTGGAAGGGGACCAATAATAATTCCACTTTTTAATCGAAAATAATCTATATAC[T/G]CCCAATAAAACTCACAGTAAAATAAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T	C	GCATAGGGTTGAGGGGTGTACAAGAGGAGGAGAACCAGATTCAGTCAGTCCATGCCTGGAGGTTAGTCTGGGGGGTT/C]CGGCGGGGATGGACACAGACACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G	T	TCAATCTGAAAACTTGCTGTAAGCCAGCATGGGGT[G/T]GGGGAGGTGATTATGGCTGGGGAAGATGGGCACTCACCCGACAGCAGCATCTAGCACCACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G	A	ACAGATGTCAGTTGTTGAATTGGCCCATTAAAGTATGGGCCTTTTCTTTGTTAAAAAGTCATTCCAAAAGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAAAACATGA[G/A]TGGGGGAGTAGGCTCTGACAGAAGGGTGGGCTGTC
WI-18261	26	G	A	GATTTGAAGGGGATTGCTTATTTATTAAC[G/A]TGAAAAGCGGTGATAGAGGAACTGTTTAAGATAAACAACTTATAAATACTCCAATTGTGAGAAGTGAAAGATTG
WI-18268	88	C	T	TAGGAGGGAAAAGGAGGTGGGCTCCTGGCCCCTCAAGACACATGAGAGAAACGGGTGGTGCCTTCCAAGCTTCCTTACTTCCCCATAGAT[C/T]CCTGACAATGTGCTGCAGAAGCCTCCAACCTGGAAC
WI-18299f	107	C	A	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTCTAAGATCATTAACTTGGTTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTC[C/A]TTTGCCAATTATTGACATATTCTGCAG
WI-18299e	101	A	G	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTCTAAGATCATTAACTTGGTTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGA[A/G]GAATTCTTTTGCCAATTATTGACATATTCTG
WI-18299d	77	G	A	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTCTAAGATCATTAACTTGGTTTGCCAATTTTTTATCTATTTG[G/A]GTCTGAGAATTCCACAATTTTGAAGAATTCTTTTGCCAATTATTGACATATTCTGCAG
WI-18299c	67	T	G	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTCTAAGATCATTAACTTGGTTTGCCAATTTTT[T/G]ATCTATTTGGGTCTGAGAATTCCACAATTTTGAAGAATTCTTTTGCCAATTATTGACATATTCTGCAG

WI-18299b	52	G	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGAAGAATTCTTTGCCAATTATTGACATATTCTGCAG
WI-18299a	48	C	T	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCTTTGCCAATTATTGACATATTCTGCAG
WI-18307	76	G	A	TCAACTTGTACCAAGTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAGTTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTCTGGTCAC
WI-18324	72	C	T	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGGTGGGGTACTGATTTATC[C/T]TAGATCCAAATAAAGCATGCAGAAGTG
WI-18350	48	T	C	ATGAAAGTCACTTCAATCATCATAAGGGTCAAGAGAGAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAAGGTGTGTATCTGCTTGCAATTTAAGAAACAACAAGTCA
WI-18395	77	G	C	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTTCCTGGAAAATTTGAAGAATAAATTGATTATTCAAG[G/C]TGTGCATTGGTTTATACATATCTCCTTCTCTTAATGCAAAGCTATG
WI-18398	62	G	T	TGCCAGTGGCAAGACACTCTCTCGAGGAAAAAAAAGAAAAACAACAGCAGAATTTGGAGGATAATTGTT[G/T]GATAACATTGCCAGTATAACCATAATTCAAACATATTCAAAGGGTT
WI-18396	21	C	A	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTCGCTCTTTCTAAAATTAAAGAAAGCAATGGAATTTAAAAGATCATCATCAAGAAATAGAACTTACACATATGTAACATTTAACTTATCAACTTGTACAAGTCAATGAAA
WI-18409a	20	C	A	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTTCCCTTTAATCCTTTCAAATTCAAAGGATCATCAAAGGAGGAGGTGCAGAAGCTCTGGGGCCCCCAAGTGCTA
WI-18442	62	C	T	AAAAAGGAAAAGAAAAGGATGGAGTAAGAGAGGACAGAGAGGAGGAACAAAATAAGTTTCTGG[C/T]TTGGCTGATCTGGGTGATCAGGTGGACACTTATCCCGAGAAGGGAAACACAAGAGAAAAAAAAGGTTTATAGGTGGGGAAGAGGA
WI-18452	38	G	A	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGGTATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTCCAACCA
WI-18489	102	A	C	ATATAAAGCTGGAGACTGTGGAGGGTGAGAGGCAGTGGGGACTAGCTGTTGAAAGAGAGAATGTAGCAGTAGTAAAGATGAAAGACTGCAAGCTGCAAGGATTCAAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAGAAAAGGCCATATAAA
EST5b	93	A	C	CTGGTGGGGAGGAAACAAATTGTGGTATATTCATACAATGGAAACTCTTCAGAAAATAAGAAGGAACAAACCACTGAATCACACAACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAAACCATTCATAAGAATACACAGTACAT

ID	Pos	Allele 1	Allele 2		Sequence
EST5	93	A	-	---	CTGGTGGGGAGGAGAAACAAATTGTGTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAGGAACAAACCACTGAATCACAACATGGACAACATCTCAAATCATTATGCTGATGGAAAGAAACCATTCATAAGAATACACAGTACAT
EST6	48	C	-	---	TTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCTGAACAAAAGCTTTCTTTCCTTTGCAACAAGACAAGCAAAGCCACATTTGCATTAGACACAGAT
EST8	158	A	-	---	GGACAGGAGACCTCTATTCCCGCCTCCGGTCGCAGCGCGCTGGTCTCCTGAGCTGGACTGAGCGCCCTCTTCTCAGGGGCGGTCTCCAGGACCCAGAGCAGCTGTCTCCTGAGTTTCCCTAGAGCTGTGTGCGGCCAGATAGCTGTTCCTGAGTTGCAAGCACGATGGGAGATTGGACACTGTGCTTTGGTGGGGT
WI-18740c	104	G	T	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAAGTGAGAACAATCTCATTTACCATCATGTATCC[G/T]ATAATTCATTTGATGGCTTCTATTTTTGGCCA
WI-18740b	96	C	G	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAAGTGAGAACAATCTCATTTACCATCATGTATC[C/G]GAGTAGTGGATAATTCATTTGATGGCTTCTATTTTTGGCCA
WI-18985a	105	C	T	---	CCAAAGTCTCCTGTTCGCTCATAAAGAAGTTTTTGGGATGGGAGAGAATCCAGACCACCATCTTGGGCAGCCAGGCCCTTGCCTTCATTTTACAGAGGTAGCACAA[C/T]TGATTCCAACACAAAACCCCTTCCCCTTTTAAAATGATTTCTGTTCTAATGCCATAGATCAAAGGCCTCAGAAACCATTGTGTGTTTCCTCTTGAAGCAATGACAAGCACTTTACTTACTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114	G	A	---	GCCAGCAGCTGAAGTCTTGACCGTGAAGAACATCAAGATACCTTTGCGTGGATCAAGCTTGTGTACTTGACCGTTTTATATTACTTTGTAAATATATTCTT[G/A]TCCACATTCTACTTCAGCTTTGGATGTGGTTACCG
WI-19112i	212	G	A	---	CCGTGTTCACACACACAATGGCAAGCATAGTCGCCTGGTTACGGCCCAGGGGGAATATGCCAAGGGACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACAACCACAAGAAACGACGACAAATCTTTGCGAGATTTCTTCTTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAGGGTGACAAGGC[G/A]TCTCTCAAACAGTTCCATACCAACTGCTTTGTCTCTAG
WI-19092	232	A	C	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGTCTCAATGGAAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCCTATAATAAGTAGAGCAACACACATTGAAAGCTTCTGATCAACGGTCCTGAAATTTTCATCTTGAATGTCTTTGTATTAAACTGAATTTCTTTTAAGCTAACAAAGATCAATAATTTC[A/C]ATGATTAGCCGTGTAACT
WI-19057i	175	G	A	---	CCCATTTATTATAGGCCAGTGATGTCTCAAAGAGTAGGACGGTCTACTGGTCTTTCAACTCCTTCAGTCTTCTGACGGCGGACTTACGGTGACGCGGAAGTGGTATTGTACGCTGCAGCCACGCCACTGTCTTCATGCAGGAACCACCAGTGCCAGATCCCCACAGCTC[G/A]TCTTCCATCTGGTTTTTGCCACA

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WI-20103	168	C	T	...	TGGGACTTCCAACTGCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGGACAGGCGGCTGTGGATATGGGAGTCCAGTCTTATCCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGGTCCTCCCCA(C/T)TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTCTTTCAGTCAACTGGGA
WI-20441	111	G	A	...	GCCTTACCCATTTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAAGGACAAGAAATGGA[G/A]TGAATAAGTACCCCCCAA CATATACAAGAAAAGTTAGCATACTTACCCCGTTTTCACTACATCAGAGCAAAATAAGAAATCTTT TAAGAAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTGGGGG
WI-19911b	116	A	G	...	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAAAATAACAATGCAATTTTA[A/G]ACACTGTTTTGAAA ACTTAAAAGTGCAGCAATA
WI-20613c	165	A	G	...	GTCCTCAAGGGGGAGAAAACTGGTTCTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAAATGGCATGGGAGGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAAGGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A	C	...	GTCCTCAAGGGGGAGAAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAAATGGCATGGGAGGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A	G	...	CAGTAAAAGAGTGATTCAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCCACACTGGAAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T	C	...	GCCCAGTTGGAATATGGCCTATACGAACCAAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAG[T/C]TGAAAAACCAACTGGAGCTGCTTTCCAAGAATGTTCTGTGTCCTTCAAATAGGAATTCCATG TTATTCTTCTTGCCTTATTCTCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	G	A	...	GAGTGCCCATACCTTCTCCCCAGGCCTTCTCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCGTAAGACCTCCTTCCCTTCCTCCAGCGCCAAACATG GCCAGACTCCTT
WI-18959	123	G	A	...	AGCAGTGGCCTTATTGCATCCCAAACCACGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTCACAGTGCTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGCGCCGCCTGGCAGTCCGTGGGGACGCGGGATGGTTCTGGCGTGTTGAGATTCTCAAAGCAGCAT GTCGTGGACACACAGACTATTTTGATTTCTTTGCCTTTTTGCAACC

WI-20146	31	T	C	TGAGTCTTCTGTAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAATGCCAAACACTAG CTCTGTATTAATCCCCATCATTACTGGTAAAGCCTCATTTGAATGTGTGAATTCAATACAGGC
WI-18922	74	G	A	TAGGAATTGGTTTCACGCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGGCCTCTAATTCACAGTGCTCTTTCTCCCACTGTATCCAGGTTCCCTCCCAGAG GAGCCACCAGTTCTC
WI-18763b	53	A	G	TTTCTGTGTGTGGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGTGA[A/G]TATTTAGAAATG TACCATATTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38	A	G	TTTCTGTGTGTGGGGTCAACCGTACAAATGGTGTGGGA[A/G]TGACGATGATGTGAATATTTAGAAATG TACCATATTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75	G	A	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A	G	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[A/G]AGATGTT GGGAACAGAAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T	C	GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTTGGTCTGTTGTTTGATGAAATTCTGAG GCC[T/C]TGATTTAAATCTTCATTGTATTGTGATTATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C	T	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTTGGTT TCTTGTATTATTTAAACGGTTGTGGTTCCTTTTTCCACGGAGGTTCAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C	T	GTGTGTCCAAAAATGGGGTCTGCTCCTGCTCACCTTGACCCTTCCTTCTCTGCTTCTCTCCTCATCA TCATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAACAAAAACGTAAGTTTCATTGGGCAAAAATTGA GC
WI-19970b	167	G	A	TATAAGCCCGAGTCACCAGGACACGGGCCTGTCTGGCCACAGAGGGGCTGCCTGTGGAGCCTGCCCACC GGCCCCCGGCCAGTGCAGTGCCAGCGGGGGAGGAGGCTGCCGCGGTTCCTGCCGCAGTTCCTGCGGGGACC AGCAAAGGCCTTCTCACTGGGTTGGTCAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T	C	TATAAGCCCGAGTCACCAGGACACGGGCCTGTCTGGCCACAGAGGGGCTGCCTGTGGAGCCTGCCCACC GGCCCCCGGCCAGTGCAGTGCCAGCGGGGGAGGAGGCTGCCGCGGTTCCTGCCGCAGTTCCTCACT[T/C]GCGGGG ACCAGCAAAGGCCTTCTCACTGGGTTGGTCAAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA

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WI-19067d	202	T	G	---	TATTGCTGCTTGTCACTGCCTGCCTGCCCAGAGAGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTAATAGTGTTCATAAAGAAA[T/ G]ACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
WI-19067c	153	G	C	---	TATTGCTGCTTGTCACTGCCTGCCTGCCCAGAGAGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG[G/C]AGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
WI-19067b	151	T	C	---	TATTGCTGCTTGTCACTGCCTGCCTGCCCAGAGAGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTG TGCACATTCCCCTCCTCCCCAGAGACTGCCCATCCCACAGATGATGGATCTTCAGTGGGTT CTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGTGAGGGGTTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
WI-19067a	57	C	G	---	TTAATCCCAGCCCTACCCTTGTTAGTTATTTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCCTCCAACGTTAAAAGACAGTGGATCATGAAAAGT GCTGTTTTGTCCTTTGAGAAAGAAATAATTGTTTGAGCGCGAGAGTAAAATAAGGCTCCTTCATGTGGC GTATTGGGCCCATAGCCTATAATTGGTTAGAAGCCTCCTATTTTAAT/CTGG
WI-19106	247	T	C	---	CAAGGCAAAATATCAGGAGGCTTTTTACACACCTACTAAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAAGGAGAATAATATTGATTCCTCACATCTTAACTTAGTATTTACCTAGCATTCAAAACCC AAATGGCTAGAAAC[A/G]TGTTTAATTAAATTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAAACAATGGCCTGGTTCAATTTCTTCTTCTTCTTTAATAAATTTAAGTTTT
WI-18944	147	A	G	---	CCCATCCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGAAGGATGATTGTTCATAATACATAAA GTTCTCTGTAATTACAACTAAATTATTATGCCCCTCTTCTCACAGTCAAAAGGAACTGGGTGGTTTGGT TTTTGTTGCTTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTA AAATAAATAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCCATCACAT
WI-18952	232	G	A	---	CACACCTCATGCTCTAGCCTCACGAAACTGGAATAAGCCTTCGAAAAGAAATTGTCCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTTGCTGATTTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAATACCCTGTACATATCTTTGAGTTCAA[C/T]CTTTAGTACGTGTGGCTTGGTCA
WI-18932d	177	C	T	---	CTTCGTCGTGGCGGTAAGAACGTGCTGTGTGGAAGACAAGTCTGTGGCTTG

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WI-19042	193	A	C	TTTGTCAGTGTTGCCTCTCGCAATGCCTCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAAGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGGACAGTTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCA[A/C]GGCTGTGTTTAGATTGTATTAACTATCTCTCTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208	A	C	ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAAAAACACTACAGGTGTTGAATGGTTAAAATGTAGGCCTCCAGTTCATTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTCGCACACTGTATTAAATGTAACTTTATTTAATGAAAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATTTATCTT[A/C]ATAAAAATGCTAAAATGTCAATTTATCACTGCGCATGTTGACT
WI-18851	90	T	A	GCTTCAATTGGCGATTGATTCAGTGCCCACAATGTAAACAGGGTTGGTAGTTGTTACTCATTTGAATATACCTTTTCCTTATTG[T/A]GTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76	T	C	TCAACTGCAGTGTTGCTTCCTCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCCACAGAGGC[T/C]GGGGGTAGCCATTGTGCAGTCAGTGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAGGTGCTGTGT
WI-18821a	69	C	T	TCAACTGCAGTGTTGCTTCCCTCCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCCA[C/T]AGAGGCTGGGGGTAGCCATTGTGCAGTCAGTGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAGGTGCTGTGT
WI-19021a	20	C	G	ACTCCTCTGCTGCTGTCCATC[C/G]ACTGTCCTTTGAACCAGGAAAAGTCACAGAGTTAAAGAGAAGCAAATTAAAACATCGAATCGGGAACACATGGTTTATCTAATAAAGTGTCTTCCATCACGTTGCTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTTGCGTGAGAGCAAGTAGCCCTCCCCTGTCACATCGTGTGAGCCCATGTATGCTGTGGGGTAGAGAC
WI-18908	70	G	C	TGGAAATTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATTCTTCCCTATCTTTGCCACCCTCATGCTGTGTGACT
WI-19037b	155	A	G	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCCTAGCCACCACGCCCTGTATGACGCGCAAATATCCCCAAAGCTTTGGGTCCTCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGGTCCCCTCCCCTTACGAACACA[A/G]AAACCCAGCCCACATGACTAGCACGCTGAGCTCTGCAGGGACCCAGTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47	C	A	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCCTAGCCACG[C/A]CCTGTATGACCGCGCAAATATCCCCAAAGCTTTGGGTCCTCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTCCCCTCCCCTTACGAACACAAAACCCAGCCCACATGACTAGCACGCTGAGCTCTGCAGGGACCCAGTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66	T	C	TTGAGGAGGTGGGGGTGAACTGCTCTTGGCAGGGATTTGTGACACTGCATTGCTGCTGGGCTGTGTTCC[T/C]CGGGGCTCTTCTGGACCTTGCACCGTGGATACCAGGCCATGTGCCATGGTGATTATTTGGGTCCTGGGGAGGGTGGGGTGAAAATAAAGGC

WI-18972a	112	A G	AGGCCTGTGCTGGCTTATGTCACCCAACAGAGAGGGTCCTGAGAAGTCTGGCTGCCTGGGATGCCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAAGCAG[A/G]TGCTTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCAGACAGTCAGCATGGAATGCTCTTGGCCA AGATGTGCTTTGCCCTGAGCAGCAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184	C A	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCATCTCAA[C/A]CTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTTGTCTTGTGCACTGTAG
WI-19016a	161	C T	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGA[C/T]TGTATACAGAGGTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTTGTCTTGTGCACTGTAG
WI-20096	21	T C	GGTTTTGGGGGCATTTATTTC[T/C]GATAGAGACTGGCACAAGCTTGGGCTAAGGACACCCGCCCCCC ACCCTCATCTAGAAACAATCTCTCTCGCCAGACTTG
WI-19591b	156	C A	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATG AGTATAAGAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTCCC CTTAGGGTGGGGAGCTCTTCCCC[C/A]CTACCACTCCCCAAGGCATCATTTGGGAGAAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCTGTTTGTTATCTTAGGGATTGCACCTTCTTACACGG
WI-19591a	45	T A	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAAT[T/A]ATAAGGTAACTCCAAGC CATGAGTATAAGAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCCTTAGGGTGGGGAGCTCTTCCCCACCCCCAAGGCATCATTTGGGAGAAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCTGTTTGTTATCTTAGGGATTGCACCTTCTTACACGG
WI-20310	125	G A	TCCTCCAGCTCTGTCATCCTTGTCTTGTGTTCTGAGGGTTCTCGTTCACGGCGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAAGCCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAA CTGGACCCCTTAACTACAAAGGAATCTTGGATGAATTATTTTAGCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTCACACTCAGGCCATCTTCCTCCCAATGTCCTCCCCGGGGG
WI-20860	224	G A	CTCTCCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTCAGCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCCTCATGCCCTCCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTCTCTCCT CCCCAGTGCTGTCACACTTGGGCAAAGCAGAGTGGTGGCAGACCAGCCTTGGCCTTCTCGGCTCTGCGCTT GGAAGGAAGGGGCGGGGCGGTCATT[G/A]GGTGATGGCCTCATCTTCTCCCCCGGGGG
WI-19359a	39	T C	GACGTGGACAAAGGAGGTTAAATGAATACTTTGTTTG[T/C]CATGTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTCGGCAATATTCCTGGGCCTCAATTGTTGTAGACC GGAACAAGGCCCTCAGAAAACAAAGGACATGCAGCCTCCCTGAGCCACGTTCCT

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WI-19766b	93	A	G	TGGCCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGGCAGGCAGGAGATGAACCATAGGAGCCAAAAGTC[A/G]GACAAACAGAAGAAGGCACACCAAGCCTGAAACCCTCCGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31	G	A	TGGCCCTCAATGACTGGTACATTGGAGAAGCTG[G/A]TGCAGCAGCATCCTTTCTGTGGTGGGCAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAGAAGGCACACCAAGCCTGAAACCCTCCGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126	C	G	CTTCCTCTGTTTGGCTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACTTTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCCTTGACTGA[C/G]AAAGCTTAGAAAGGAACTGAAATTGCTTCTTTGAAATATGGATTTTAGGGCGGGGCGTGGGTGGGCTCACGCCTTATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGTGGGATCACCTGA
WI-20512c	59	T	G	CTTCCTCTGTTTGGCTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACT[T/G]TCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCCTTGACTGACAAAGCTTAGAAAGGAACTGAAATTGCTTCTTTGAAATATGGATTTTAGGGCGGGGCGTGGGTGGGCTCACGCCTTATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGTGGGATCACCTGA
WI-19599	230	C	G	GGGCCTTAAAATTCCCCTCTGTTGGGGACTGGTCTCTCCAGTTTACAGCACAAAGGATCGCACCCTTTCCATAACCCCTTCTACACATTGGGAAGAGACACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACGGACAAAGGTAAATCACAGACGTAAATCACAGTGTTGGCTCACACGTAACCAAACACCTCTTTTTCAGAACAGAGAGCGTTAAAAGTAAAGGGCA[C/G]TTCCAAGAGTAACAACTGCTA
WI-20679	82	T	C	TGTTTGAAATAAAAATTTCCCATGGTCTTAATTGAACTGTATGTTACTTTCTTTAGAATATCCTTTTTTTCATTAAAAATAATT[T/C]TCTAAACCACTCTATGTGTTCAACCTTCTGTTTAACACTAAGATATGGGTTTTTGAAAGGCCAACAAGTCACCAGTCTCCATGAAGTGGGCGAATTGGTCCTTGTTTTGGAAAGCTCTCCAGGGTGTTTCTCCAGAAA
WI-19909a	29	T	C	CCAGAAATAAAAGCCTGAATATTCTCTTTC[T/C]TTAAAAATATAATTTTTTCCTTCTTCTTTGCTCTTCCAAGTAAATCTTAAAATGAACCTGTCTATTTTAATCTAGGCAATTATAACACTACCTAGGCGGGGTTTTTCCTTTATACCTTGTTCTGTGTACTGTGGAATCAACTAA
WI-20341	221	G	C	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGGCATGAGAGACATTAGGAAGGCCACAATTATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTGTTTAGCAGGAGGCAGGAAAGTGATCTGGGGGTCTCTGGCAGCAAAGCGTGTGGTAAATATTTGGGTGACGTCATGCATCCCCCATGCATTGGTTTTTG[G/C]ATGTCTCCAGTGAGCGTGTTGGGCAAGTCT

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WI-20113	60	T	C	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAGACCTGAAATACT[GT/C]GGAAACAGTAAAAGCAAATTACCACACAATTAGGAGGAATTATTTCAGACATAGGATATTTAAAACATCACTCAAATACTGGAGCATGATTCAGCAATAAATTCTATTCCATAAACCAGGTAGATAAATGTCACAGCTTTAAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107	G	C	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAAACAAGAGAGCAGCGGCAGTGCAGCGGTGTGGCCACTTCCCCACCAGCCAAGCAGAACACTTGACTTCATTCAGTTCAA[G/C]CTTTACTCTGTTACTTTTTCCTCCCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTCAAGGTCCTAGGAATATAACTGGTACTATAGGCAAACAGATGCA
WI-20721	72	T	C	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAAATCATACTTGATTTAACCACCTTCAGAAATTCTA[T/C]AAAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A	G	CTGGATTTTAATATTTCTGGCCTAATAACCAAATGTAATCAATAAAATTGGTCAATATCTCCACCTCATTTCTGCTAACATGTTTGCAAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAAGTCATGAGACCCTTAGCTGATCTCAT[A/G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAAGCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C	T	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCCACTTCTGGCGGTCGATGAAGAGACTGTTGGTCATGGCGGTGA[C/T]GTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGGAACTGCTCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G	A	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCCACTTCTGGCGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTTCTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGGAACTGCTCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A	T	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTTGTAGGCCATTGTAACACAATGTTAAAAGGTACAGTAAAAATACAGTATTA[T/A]ATCTTATTGTGTAGCACGGCTGTGTGAGGCTCATTGTTGAATGAAGCATCCTTAGGCAGCACGTGACTGACTGCAGATATGTGCTGCAAGAACTTTGCCTT
WI-19641a	46	A	G	TCCAATTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATAGTCTCATGTTTTTAATTTATGAATAACGTCTGATTCATTGATTTGTATTTGTATTTACAGAAGATGTCAGGGCTATCTCATTCAGTTATTAATAAATATGGATCAGAGTAGTAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTAAAAAATACTCAGAATGAGGTAGTATTTTAATTTCATCCACCACTTG
WI-19642b	52	C	A	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT[C/A]GGGTAAACCAGGACTATTGCATGAGCATTCTTAATACGTATTTTGATGGACACAAGTTTTCATGTCTATTA
WI-19673b	180	C	T	TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGCCTTACTCTCAGTGAGTGCTAGTGGATTTACCTACCCCTGCTTTGCATCACCACTACTGTTTAAAATTTAAAGTTATTAATAAATAATGGATCAGAGATGGATTTAATTGTTTAATTTTTTC[C/T]CTTGGACCAGCTGAAAGAACACAGCCC

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WI-19673a	35	G	A	TCTGCCATGATCACATTGTGATGAAGAACATGATG[G/A]TCACTAGTAGTAGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCTGCTTTTGCATCACCACTGTAAATCTAAT AGTGAAAAGGCAAATGATGTGTCTCAGTATGTCTCAAGGTCCACACGTCAAAAAACACAGCCC
WI-19724	35	A	G	TTTATTTGGGAAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196	T	C	TCCTCCTCCCCCAACTAGATGGTATTGATCACTCTGCCCACAAATGGTACCCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCTTCATGAGAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGCTGT GGTGAACTGCAAAGAAGAAACCAGCCAATGTATTCCATAGAGGCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTGGTGTTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	CTTTCCCTCATCCCCTCTTCCACCACACCATCCGGAACAAGTGCTCCAGGATTCCTGCCCACTGGC CATTTTGGAGTGTGTCC[A/T]TTGGGTAGCAATGTGAAACCACCAGGGCCTTTGTTGGAGAAAATGG AGGGGGTTGAGGGAGTCCCAGGAGGGGCTTATTTGAGGGCGTTGCCACTTGCTCATAGGCGGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATTCTTCCCGGGCGTAGGCA
WI-19946	122	C	T	CAATGGACTGAATGAGTGCGTGCTGCTGGTGGGCGCACACCTTCAATACACGTCAAGGTCG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTGAGACGCACAGAGAGGT[C/T]TCTTCCTG ACCCAGAGCGCACTCACGAGCCCAGGTCCTGGTTTCAAAACTGCATTAACCTGCGCCCAGAGAGTTCAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	CACAGCATGGTGTAAAATAGCATCAGATTGAATGAAAAGTTTGTTAAATGCAACCATAAAATAATTATA ATAAATATACATCAAGTAACTTACAGCACCACGTTAGCAGCAGATACCTTACAGCTTGTGTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTGTGTCATCTCACTCAA GTGATGGCCAACAGAAGCTTCTGAACTCCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40	G	A	TTGGTTGGATACTTGCTGGAAAAAAAAGCAGTTTAAT[G/A]GTATTCAAAATACCTTTAAAAA GTATTCTAGCACAAGAGATTTTCTGTAAACTAGATTATGTTGTAAACTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTGCGCGTCCTGAAAACTGCGAGA AAGGCACTTGAAAGCTGTTTCTTTAAGATATGGGATTTCTTTTTATTCTT
WI-20218	26	T	C	CCACACACTCTGGTTTTATAAAGCTAT[T/C]AGGACAGAGCAGAGATGGAACTGAAAAAACAGGGTAG AAAATAACATAAATTGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCCA GTCAAATACTTTAGTCCCTGCGAGCAGCAGAAGATGCCAACCAAGTCTCTATACTGGCTGGGGGATCCTGCC ATGGGATGCAGGAGAAAA
WI-20295g	154	T	G	CAACCTTTTTGACAAGGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTAATATCTCCAGGCTTGATTGGGGAGGGGCTGGGCTTCACCCCTTCTTCTTTCCA TCCAGTCTATTGCCAGAT[T/G]CCAGAAGAAGCGCGGGAAGCCCAGCTCTCCAGCCACTATAGCCACTGTGG GTCGGCGTTCACCTTCTGTGTCTGCGTTCCCTCATGCTGGGACTTGTCTTTCGGGG

WI-20361a	192	G	A	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTTAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCCAGAGTTACACTCTGCACTCCAAAGCTA CAACAGTGCCACAGCTGAGAGGTTCCTATACTTCCTACTACTGTGACAATTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A	G	---	GAGCCAAACCCAAAACAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCT TCAGAATT[A/G]TCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA AATTTCATCTTCTCAAATTTAAAATTGTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATA AACTGCCTATCAGGTATCATCATACCTGCAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G	A	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTATAAGTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAATAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAAATGCTAAAC[G/A]GGAGCCGAGCTCTTCCGCATTCAGG
WI-20593	79	A	G	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTCAGTCTGTTG CTGTACTTCAG[A/G]TTAAAATCTGGGAATGACATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCTTCACCAGACTAT CCAGAAGCCATTCCATGGGGTATTGGTCTCGCATACTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATTACCTTGTCCTCA[T/C]ATGTATCT TGTCCCTGCTGTCTTTTAGGTTAGCAAGGTGTATGAAATACTTTTAAGTTTTGTTCTTTTCCTCGT GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGGTCAATTACAAAATTGCCATGGAACTGAGC AAAAGGCCCACGTGGGATAAAATCACTCACCATGACGCCACCAGTATT
WI-19066i	239	A	G	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCTGTGAATTACTTCTCCATATTC[A/G]TTTCTTTTA ACCATTGCAGGCAAACTTTTCTTCTTAAACGCCTTCACT[A/G]TTTCTTTTA
WI-19066g	184	C	T	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCG[T/C]GGTCACCTGTGAATTACTTCTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066f	148	T	C	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCG[T/C]GGTCAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA

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WI-19066e	147	G	C	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCGTTCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGC[G/C]TTGGTCACCCTGTAGCTGAATTACTTCCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066c	100	G	A	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAACCTTCAGCTGATC[G/A]TCCTTAGCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066b	87	C	T	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAA[C/T]CTTCAGCTGATCGTCGTTCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066a	72	C	T	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCA[C/T]TTAAAACCCATGAACCTTCAGCTGATCGTCGTTCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-20660	105	G	C	---	TTTACAGCGAGTTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAAGAAAATGTGTGTCTAAATAAATCTCCCTTTTGAATGTATATTTGT[G/C]TTAATAAAGGGAAGCATTAATATTACAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAAAAAGCTATCCCACCCGCGCCCCAAAAAATACTGTTTAACAACACTATGTTTTAAGA
WI-18768	120	C	T	---	CTGCTGCCAGCTTCTCTCTTGGCCCTGCTCCCAGATGGCGGTCTCCTGGCAGCCTCCCCTCAGTCTTCCTCCACCCGCCCTCTTCCTTCCCCAGCCTGCCTGCCATGTGCACCCTTGGT[C/T]TTCGCTCCATCGCCTTGAAAGCTCTGAA
WI-19087	37	A	G	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[A/G]TATTTAACTTCTAGTTGCTCTTGCTTTGGTCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGCCTTTCCATAAAGTGTAATTTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGCAGTGGCCCATCCAGCATGGTGTGTCTCTTATCTTGCATCTACCTGTCC
WI-18790	49	A	T	---	GAAAGCCAGAGATTAGCCCGCATTCGGCATCCGCCTCCGTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGCCACTTGGGAGATCAGAAAATTCATATTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCT
WI-18987	35	G	A	---	AGGAGGCTGTTCCAGGAGTCCTGCCCAGCAGCCTC[G/A]GTGGCCAAGCCAGACACTCACCCACCTTCCCAGTGGCCCCGTGGCCCCGTGGTCCTGGATCCTGGCTCTAGGCTGGACACAGGATTCAGACAGGATTCAGACAGAAAGAGCCAGAGGTGGACCTGAGTGTCGGTCACAGATGTGTCCCCTACACTCAAGGCTCAAGGCCTCAGGAAAGTCA

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WI-18919	26	C	T	---	TGGATGAAAACCACAGGGATTCCGGA[C/T]GCCAGAGACCCCATTTATACTTCACTTTCTCTACAGTGTTGTTTGTTGTTGGTTTTTATTTTTATACTTTGGCCATCACCACAGAGCTAGATTGCCCAGGTCTGGGGCTGAATAAA
WI-18741c	64	G	A	---	CTTTCTGGTCAAGGCTTGGACATCTCTTCAGTCATCAGAACAGAGTATCTCTGCTCTAGACCTC[G/A]CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G	C	---	CTTTCTGGTCAAGGCTTGGACATCTCTTCAGTCATCAT[G/C]ACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T	G	---	CTTTCTGGTCAAGGCTTGGACA[T/G]CTCTTCAGTCATCAGAACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G	A	---	TCAGAAGCAGACATGGCATCCATCGTTCCTCGTTCCTTGTTGGTGTGTACCTTTCACGAGACCTGAATTTTAGAATTGCCCAGGTCTGCCAGAGTGAGTGAGTTAATTCTCCTTCAGGTAAAGATAGGCTATCTCAACACTGCTGAGTGATTCAATAAACATATCAACCA[G/A]ATAGCATTAACCCATTTATTTCCTGTCCTTAGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T	A	---	CCAAGTTGCATCCATGTTTGATTTTCTGATGAGACTAGAGTGACAG[T/A]GTTTCAGAACCCAAATGTCCTCAGTAGTTGGAGCATCTCTATGAGATGGGATTATCAGATGGCCTATGTAATATCAACATTAACACATTATCAAAGTCCTCTTACAATTATTTCCGCAGCATGTCAGCTAAGTAGACCCAATGGGGAGAGAAAATGCCTGCTTCTTCTTTCCCTTTTCTCCACTGCCATAT
WI-19183	210	G	C	---	CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCTAGACAGGTAAAGCACACATTGGATGGCAGCATGGGTTTCTTCCCATTTATGGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATTATTCCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTTGCTGAGTCAAGCAAACACTTGCCTGCTCTGCCCCTTGGAG[G/C]TGCATTTGACCTGGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T	C	---	TTGAAATCCCAGTCTCCTGGCCCCCAGGCAGGGTCTGTCACCATAGAATGTCTCCTCTACTGGGGTCGTTCTGGCTTTTTGTTGTAGAAACTTGGTCTGAGATGTTCTTCCCGTGTCCATTACCATTGCGATGTTCTTTGTTCAGAGCAATGTTCTTGTATTCTGAAACTGGAAACTACTTAAATGTTCTCATCTGTAAGCATACT[T/C]CTCCTGGCTCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T	C	---	GTCTCCCCAGAGTGCTTCTGCACCCCAGCCCCTGTCCTGCCTGGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTGTCTCTGCATCCCTTCCCAGGGGGTGCCCAAGCTCATCACACCAGGGGCCATCCTTCTCAATACAGCC[T/C]GCACGGTGAGCAGATGAGCGCCCAAGCTCATCACACCAGGGGCCATCCTTCTCAATACAGCCCCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTCCTGTGTGT
WI-19135	20	G	A	---	CAGTTACCCTGCTTTGCCTC[G/A]AAAGTGTCATCAATTTGTAATTTAGTATTAACTCTGTAAAGTGTCTGTAGGTACGTTTTATATATAATAAAGGACAGACCAAAAATCAACCTATCAAAGCTTCAAAAACTTTGGGAAAGGGTGGGATTAAGTACAAGCACACATTTGGCTTACAGTAAATGAACGTAGTCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A	---	TACACAGAGGGTCGCACTTGGACTCTGAGCGGTTGGGTGTGGAAGGGGGAAAAGG[G/A]GATGGGAGAC CTGCTCCCCAGCTCTTCCTGTCACCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAGGT CACCTTACCCTTTTCAAGGGCAAAGAACTCGTGGGAGGATGTCTGTTGTATGTAATACT AATCTTTCAAGGGCAAAGAACTCGTGGGAGGATGTCTGTTGTATGTAATACT
WI-19144	222	G C	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCAGCCTTCTAAGG CTCAGCCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATTTCATTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAAACCCTCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGGG[G/C]TGGGAACCAAACACCTTCAGTGCTGGTG
WI-19139b	110	C A	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAG[C/A]ATTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGGAAGCCACCGTGCTTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGGTGTCGAGGCTTTGAAG
WI-19139a	66	C T	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAGCATTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGGAAGCCACCGTGCTTCTCTTTGG GGGGCCCGCGAGATCTAGCATCTCTGAAATCCTGGCTTTGAAG
WI-18910	112	T C	---	GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCT CATCCCAGCAACCTGTCCTTGTGGGGTGATGATCCACTGTGCTGCTTGT/C]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G	---	TTCAGGAGGTGGAGTTCGTCGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCTCTGT CACTCAGCCTTGCCTAATTGTTCACAATGGTGGAA[A/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCGCGGTTCTGCGCACTA
WI-19222	179	C T	---	CGTTTTCCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTTCTCTATGTTTTCTGTTAGGTGAGTGGTTTTTCCCCCCACCAGGAAGT GGCAGCATCCTCCTTCTCCCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGGTACACTGTCCAGCGTGTCCAGAAGCAGCACTTT
WI-19117	134	A G	---	AAATAATGCAACGCAGGAGGAGAAAATGCACTCAAGACAAGAAACATTCTCTCATGAACATTG ATCTGTTTTACAGGAAGAAAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAAATTGCATGAA A[A/G]TAGCTATTTTTTTCCTAAGACATTTTCATTCATGAAATATTTCAAGTTTTCATACTGTACA CATTTCTTAAAAACACATGATACCAGCAGCAACTGAAGTGCCGAATTTG

WI-19134c	263	C	T	---	CTCCTGTTCGTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAGCAAGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCCAGGGGCTAGAGCCAGGATGCACGGTCACGGTGCCGCACCTGCTCCTCCTCACCCTCGGCACCTCGGCTGGGTGGGAAAGGG
WI-19134a	162	T	C	---	CTCCTGTTCGTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAGCAAGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCCAGGGGCTAGAGGGAT[T/C]CGACGGTGGCTGGCCAGCTGCACTATCCTTTTCAGAGCACTTCATCCACTTGCTCCTCCCCTACCCTCGGCCACCCTGGGTGGGAA
WI-19224	112	C	T	---	GGTTTCACCAGTCTTTCCCAGGGAACTCCGATGAAGTGTTCAACAAAATGAGCGAGTGAACCAAGAAGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCT[C/T]CAGGATGCCTGTGAAGAAAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAGACTTCCAGGGAAACTCATTCAAGGAGGTGAAAATGATGACTCCTCCAAGATGAAAA
WI-19201	179	T	C	---	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTTGTCTTTGATGGCATTCTCTTCTTCCACCTTGTCTTCTCCTTTGCTCCTCGTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCCCTTCCGCCCCCACACTTGCCTGCAGGTGCACCGAAAGGAC[T/C]TGGGGGATAAAATTCAAAAAAGTGTGATGTGCTGCTCAGAAGGTCAGACTCCATGTCTGCCTCAA
WI-19034	45	T	C	---	GAAATGGCTCCACTCAGAGCTCACCCCGGTGATGAGGATAGGGGAA[T/C]ACTTCTATTACATTAAAGGCAACAGCAGTTAGTAAAAGGTTTTACAGTGTTTCTGCTGTTTGAAAGTGCAATATAAATTTTTGCTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGACATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTATGTGTGCTATATA
WI-19102	25	C	G	---	TGTTCCTGAGTCACGCTGAGGAGAG[C/G]CTTCACTCAGGAGTTCATGCTGCAGGATGATCATGAGTTCATGCCGACGTATATTTCCTTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCTTGATTAGTATCGTGAGTTTGAAAAGTTCTAGAACTCCTGTAAGTTTTTGAACTCAAGGGAGAAGGTATAGTGGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACACAGAAATGGG
WI-18548b	65	A	G	---	AAAGGAGGGAGAATCTTTTTTACATAAAATGCCTTGCATCATCCTCCAGTCCCCCTCACTGGGGGAA[A/G]AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G	A	---	AAAGGAGGGAGAATCTTTTTTACATAAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGG[G/A]AAAAAAAGCATCTNTCAAGTCTNTGTCCAACTTTGGCTGC
WI-18700	97	T	C	---	GGCAGCAGCTTTTTAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGTTACACCTGAAATCTGCTGAGAGCAGAGCT[T/C]AAGATCCACAATTGCAAGGCCACTGCTGGCTCACTTCCTCACA
WI-18501	121	C	T	---	CAGAGGGAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGTGCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCCTGCGCAGGACAGAGAGGGCG[C/T]GGACAGCAGCGGCATGCCACAAACATTCA

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WI-18017	87	C	A	ACAAAAGAAAATGGAAATAGGTTTGCGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCCNGGAACA[C/A]ACTGCTGGATAAAATCGTTCATTAAAATTATATCTCTTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101	A	G	TTATTGCGTTCCTTCGGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTCAGAAACCNTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAAGGAAGATGA
WI-18254	64	T	C	TATACGGATCATGTATTTGTGTGACCACCACTACCAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]GCCAAAATTCCCTCTTGCTTCCTTGTAGTCAGTCCTTCTCCCAACCCCAGGNACTTGGCAACCTGTTT TCCGTTCCTAGACATTT
WI-18265b	117	C	A	CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTCTTCAG
WI-18295	40	C	T	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATTCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T	C	GGGCAAGAGACAGAGAGATTTAATTGAATAAAAACTCCAGGCTGTGACACGGGTGGGAGACAAA[T/ C]GAGTAATTAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGGAGGAGGGCGTCTTTCA
WI-22585	56	A	G	TTTATTTAAATTTGCATCCTGAGATAATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCAGGTATCCTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A	G	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTGGC[A/G]TCGTGTGTAGAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G	A	GCCTTTGCTCTTTGCTGTCCTCAGAGGCCTCAGATGGATACGGCAGCAACTTCCTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAGA[G/A]GGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTGCACAGACAG GGAAACAGGC
WI-19888a	98	C	T	GGCACGATTCAACCCATAACAGAGAAATAACTCCTATTGGAAACAAGGTTTATTTGATATGATG AAAATATTTTGGAACTAGAAGTAGCAGTGA[C/T]TTGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCATTTAAAATGGTAATTTCATGTTATGTTATTTCACCTCAATTAAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C	T	TGAGACCATCCTCCTCAACAAAGAATCAGTTCAGCACCTAATTTTCCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T	C	TCAGAATTGCTTTCCACTGCCCAAACCAAACCAAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAGAAGGTACCTTCCTTGGGAGGTTGCATGACAGGATTAGTCTTCTCTGTTT/C]CTTGGT GCAAGTTTGAACCAGTGATTATGTACCATTGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI-20561b	94	T	C	---	CGTTGCTTATTAAGATGGCTGTGTTTATAAGTATAAAGCAGTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGT[T/C]GAATCAATGTCTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25	A	G	---	CGTTGCTTATTTAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69	T	A	---	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A[T/A]ATAAATCTATATATATTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCACCAGTCTGCCATCAGTCTGCAATTTCCCCGAGATAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116c	59	T	A	---	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATATATTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCACCAGTTAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116a	22	C	G	---	GCTTTCATTTCTGTCACCCACC[C/G]CTGTCTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATATATTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCACCAGTTAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20466b	133	G	A	---	AAAGATTTGCAGTCCTGGGACACAGTTTGGAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAAGATGAACATAATGAAGTGAATAAACGC[G/A]TGTGAACTAATAATGTTTAAAAGTTAGAGCTTGTCTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTCTTGCTCTTTATCCCTTCAGGTTCGATT
WI-21444	39	A	G	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTTATGGGTATTTCA GTTGTTAACAAAGTTAAAATACTTATTGGAACTAATTCTTGTATTTATTCGGAGGAGAAGAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T	C	---	AGAAATGGACAAGTAATGATGCAGATGATTTGTGAGCATTTGATGAGAAAGTGGTAGAAGGATACAG CATAAAATTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGAGATTGGATAGA[T/C]GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205	G	A	---	GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAATGTCAATGTCAACATACAAGCATATTACCTCCCCCCTTAAGTGACTCATAATTC ATTACTTGTGTCTGTAGCTTTAAAAATGTGTAGCATTAAGTGGTATTTACTTACTTGAGGGGCA ACA[G/A]AATTACGGCTTAACAACACTAAAATCATGAGGGATTG

Clone	Position	Allele 1	Allele 2		Sequence
WI-21805a	45	A	T	---	CAACTGCTCTGAGGTCTTCACTAGCTGATTTATAATCCTATATT[A/T]AAAAAAAATCTATAGTCTGCAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTTTTGTTTGCTTTTTGTAGCTTAACTGCTGTTTAGNAAATCCCAGAGGAATATGATTGAGGCCAGAGTTACATTGGTTCATAAAATTCGAACAGCAGTTGAAGGCTGTTTTTGTTAATTGCTG
WI-21778b	155	T	C	---	AAAAATCCATAATTATTGAAACCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGACTCTGCCCGCGTGTCGTTCGTTCAACTCCAGTCTGTCAATGCCCCGTCTGTAGGTGGGGTCCCCAGGTCTGGGCTTCTGAGGTCCT[T/C]CGGTAGAAGGAGGGCAGGTGGT
WI-20907	241	A	C	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCTCAAATGATCTAGAGCTCATCCTTGGGCGTACATGAGGGCAGTTGTGTTCTAGTACCCATTAGCCCATGGCTCTTCAAGCCAATTCACACTGGGAAAAACACACCCTCACAAGATGCCTATCCATTTGAGTTCATACAGGTTTTAGTAGCTAGAACTAAAAAACATTTTA[A/C]AATTATCTA
WI-21449b	222	C	T	---	AACAGCAGCAGTCACTTCCAAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTATAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAAATCACGCAGCACTGGAGGGCGGCTGGAGAAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAAGTCCCAACCTGAGAGGTCTCCACACCCAAATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157	G	A	---	GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCGACTCCAGCCTGGAAAACCTGCCCTCCCATCCCCCTTAGCGCCTTCTTGGCCTTCCGGCTGATTTCTTCGGACCAGCCAGTTCTTGGCCAGGCAAGGAGCTGTGGTGGGGGCGGCAGTAT[G/A]AGCCAGGGACTCCCTTCCCACAGATGAGGGCCTAGGGCTGCAAAAGGGGCCCCGTGAAAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-221187b	178	G	A	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTCGCTAGCAGAGCTCATGGNGACCAGTCCTGGCCGGCCTGACCAATGGCCAATGGTGATTCATTTAAAAACCAAAACAAAATACCAAGAACAGATCACTTGCCCATGGACGACATCAGTAATCTATTGGTAATGGTG[G/A]AAATTTCATGAAAATTTCCCCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-221187a	110	C	A	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGCTTGGGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAAACAAAATACCAAGAACAGATCACTTGCCCATGGACATCAGTAATCAGTAATCTATTGGTAATGGTGAAATTTCATGAAAATTTCCCCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-21609b	146	G	A	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTCGTTCACAAGCTGTAAAAACAAGCCCAAACCCAAGAGGCAAGAGCAGCAGTGGCCAGTGGAGAGGAGCCTGTAAAGGATGTTTCAAAAG[G/A]AGGGTCCCGGCTATGTGGGCCCACTGGACTGAGTGAGTCCACTGGGATGTGGCAGCAGTGTAGGCAGCAGTGAGCTGAGTGAGTCCAGGCTTTCGGGTCTGGGGAAGTGGCAGGGCTGAGACANTGGCCAAAGACANTGGCAGAGAGGAGTTGGAG

ID	Pos				Sequence
WI-21609a	42	C	T	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAA[C/T]GTGCAGTCCGTTCACAAGCTGT AAAAACAAGCCCAAACCCAAGAGCACATCACAGAGGCAAGCAGTGGCAGTGAGAAGGGAGCCTGTA AAGGATGTTTCAAAGGAGGGTCCCGGCTATGTGGCCACTGGATGGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104	T	G	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCCTTTGTGATCTGT[T/G]ACCTCACCCATGTCTCCCACCTNAGTTCC CACATTTCCCCCACGTCTAAGGGCAGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139	A	G	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTC[A/G]TGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121	A	C	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58	A	G	---	ACAACATGCCTGTTCACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATTGCACCCTTGAAA AA
WI-18829b	35	T	A	---	ACAACATGCCTGTTCACAGGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATTGCACCCTTGAAA AA
WI-20964	87	G	A	---	AGCCAACTCAAGGCCAAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGGAAGCAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTAA AAGAATACTAAGATTAGATGAACAACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAGGAAC AGATGTTAACAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	T	A	---	CTCTGAACTAAAGGCCGTGAAAGGCCATGATTGGTTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCTTAGGT
WI-22130b	165	C	T	---	TGTTTTTGAGGGCTGTGTAGCAGACTACATAATGAGCGGTGAAAGCGGCTGCCTTCCCCTCTCCTGACAC CAGCAAGGGGGAGGGCACCATCACCCGCGCGCTTGCT[C/T]GTGTTTAATCCAGGTTAAGCTATACGTTTAA GCCAACGGCGAANAGGACCCCGCGCGCGCCTTGCT ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

ID	Position	Allele 1	Allele 2		Sequence
WI-21661	117	G	C	...	GCTTAGTGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTCCAACTTTAGAATGTATAAATAAGAATGACATTTAAAATAAAATA[G/C]TTTAGTCACAGTCACACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTGTGCTTCAGCTATGAAGGA
WI-21980a	25	T	C	...	TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAAGGGAGATTATAAACCAGAAAATGTGTTTTCTGGGAACCCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTCATGGGTGAAGCCCCTGGGATAAAG
WI-21636	71	A	G	...	TGCTTGTATTAATGTGGTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAAATACCAGCTTTTTAAA[A/G]TAGCAATATCTATTATTATATAAATATTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGTGTTGATTTTGCAGAGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G	A	...	TTGCTATATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGACAAACAGTAAACATACTGGACACGGTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCAGATTAATACCTGGGGCCAAAACCCACTGAACTCACCCCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97	C	T	...	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTATAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGGTGTCCTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-21524a	35	A	C	...	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATACTTATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGGTGTCCTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-22652a	32	G	T	...	TTACCTTCCAAACCAGGCCACTTTGGAGAAATGCTATTAATCAATAAGCCAAGAC[G/T]AAGAGAATGTCTATTAATCAATAAGCCAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATCACCATCATTCCTGCCACAGAACCTTTGCACATGCTGCCCTCCCTACTCCGCCACTCCGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCTTTAGGG
WI-21703d	197	A	G	...	CAACAGGCTCATGGAACAGGGATCCAGGAGCATAGGAGGTTGGTGCTGTGGGCAGGGCTCTGCATCCCCTTCCTCACCACAGCCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCACTTGTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGGCAGAGCACAGCTAGGGCACGGCAAGGAACTTAAGGGAGGAAGAG

ID	Pos				Sequence
WI-21703c	134	A	G	---	CAACAGGCTCATGGAACAGAGGCCTAGGGATCCCAGGAGCATAGGAGGAGGTGGTGGCTGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTGCTGGGAAAGCAGCATTGGAGCCTACACC[A/G]CTTGTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCACAGAGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGCAGGCAAGGGACTTAAGGGAACTTGTGGGGGAAGAG
WI-22663c	139	G	A	---	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCGGCTGGCGGAGGTGAGCCGGCCGCTCGCTAATCTATTC CCAGTCTCGGTGAACATGGGCTCAGTGTTGCTGAGGGCTTTTCCTGAATCCGTGTTGCACTTACAG GC[G/A]GAAAGAGCTTCCTCATTTGCTGGGGCTTTTCATTTGCTGAGGGCTTTTCCTGAATGTGGGT
WI-22663b	55	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCCACTGGCCGGAGGTGAGCCGGCCGCT[C/T]GCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCAGTGTCTCCCGGCTCAGTGTTGGGGTTGCACTGGTGCACTTAC AGGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATGTGGGT
WI-22663a	38	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCCACTGG[C/T]GAGGTGAGCCGGCCGCTCGCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCAGTGTCTCCCGGCTCAGTGTTGGGGTTGCACTGGTGCACTTAC AGGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATGTGGGT
WI-22668	99	A	G	---	TCTTTATCCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATATT[A/G]TTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTCGAAGAAACTTTTATT
WI-22631a	52	T	C	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCTGA[T/C]AGCACCATTTT CAAGTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTTGTAAAATTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTT
WI-20258	157	G	T	---	AATCCACACACTTTCACGGAGGGGGACCAGCCTGCCATGTCGTCCCCAGGCTCACAGCAGCGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGGCGCATTGGAAACCGTAAGGCATGACAACG GGAGGCCCGCGGGGTGTTTCAG[G/T]TGCGGTTGACGGGCATGCGCCGGCGGCCTCTCACAGA AGGAGGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212	C	A	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTTCCACTCTCTCCTGCTAACTCTGACAGGAGTGTTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGAATCCTTAACAAGCTAGTTGCT ACCAACCCCA[C/A]TGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	---	TGGGGCTACTTTAGATGGGATGGCCGTCAGGGTGCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCAGCAGCCAGTCGTCGAAGCCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACTTGGGCTTGTCCTACAGGGTGAAAGGCGGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A	G	---	TGATATGATGTCTGAGATTGCTTGCAAATATGCCTAGGAAGGGAAGAAGAAGTGTTAGAGATATAGGA CAAATCAAGAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTT TGGGATATGTTTGGGAAT
WI-22750	48	G	A	---	TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT
WI-22775a	60	A	G	---	TGCTGTTTCTTTAGTTCATGACGTTTATCACAATGTCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAAAATAAACTCCCTAAGGGCAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C	T	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAGTCCTGAGGGAG CCTAGTCCTCCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G	A	---	TCTCTCGTGTCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCCACCACACGGTGTCCCACATT CCCCATCCTCCCCGTCTGCTCCCCATCTCAAGTCCAAGGCCAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAAGGAGGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGCGCTGTGGGTC CTT[G/A]TTGGCGTGGTGATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C	T	---	TTGAACACCTGACCTCTGACCTGACATGTGG[C/T]TCTGGTCCCCATTGTCTCCAACGGTGGCACA TCTTCATCTTGTTATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAAACACACA
WI-21314	122	A	T	---	CCATATCCAGTCTCTTCTATTGACTTTAGGGTTCAGTTATTATATCCTTATCACTAT GACTTTCATTTGATTTTTATTGTTTCTTCCATTTCTGTCAAACTTTC[A/T]TTTGTTTATAA ACTGTTTTCTAAACTTCACTTAATTCTCTATCTGTATTNCTTGAGTTCCCTGAACTTCTTTTAGAGG
WI-21186	95	G	A	---	AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAAACAGACTTCTGGACCCAACCCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGGCTTAC[G/A]AATTAGTATTTCGAAGAACCTTCCTAAGTGTTGCAG ATGCTGCTTGTCCCGGGAACACACTTTGAGAACTATTGTTCTAAAAATGTTCTCTCCTTTCTTTTAAA GGAGAGACAGGAATTCCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A	G	---	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATT CATTTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTGATCAGAAACTCTGAGGGTGAGAGACCAAGCAACCTGT

ID				Sequence
WI-21190	39	T	C	TTTTCCCCACATACCAATGCACCTGTTTGTATAAACTAT[T/C]GTGGGGTAAGCCCTTCTTGGAGAC CAGTGACATAGACATGATGATCCCATTATTATTATAACAAATAATTATTAATATCTGTACTATTACTGC TTTAGTTATCTAGTGTTATTGAGAAAGGAGAGAAGTCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186	G	A	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGATGACATTGGTGTGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C	T	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGATGACATTGGTGTGTGTTCCTCAGCAAGTC[C/T]GTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C	T	GAAAACGGGGTGCTAAACAAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAATTTCAGAGCCTTCAAATACATTCTGGGG TCCAATCACACTACTTCAGGTTCAGACTCCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCTCATTTCTACAGTCTGTATT[C/T]TTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C	T	TCACTTTGATCATAATCCCTGTAAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTCC TTATTCAAATGTCACAGCCTGACGCGTTACTGTACATATGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGAGCGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53	A	G	CAGTTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACTATTCCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G	T	AAGGAAACTGCATGGGTACAAAT[G/T]TTCCAATTCATCATTAACAAGGTGGGGAAACGGGGTCATTCT TGGCCTGCTCCCAGAACAAGGGGCGAGTCTATGCACTCCTG
WI-21059b	181	T	C	GGGGACCAGGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCATTCTATTTC[T/C]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C	T	GGGGACCAGGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]T GAACTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

ID	Pos				Sequence
WI-20442	37	T	C	---	TCCACGTGAAGGAAGAAAAAAAAANGGGGGGGGGCT[T/C]TAAGGTGGCACAATTTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAAACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43	T	C	---	GTGACAAGAGGTGAAGCAAGGGACAAGGGCAGCAGGGCAGTC[T/C]CTCGGGCGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T	C	---	ATCAGAAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCTACATCTGGAATT[T/C]CATTAC ATCAAACGTTAAATTTTGTCCGACCAGTTCTTCATTGCTGATCACTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAATGAATATTTACCTTGTGCTTTCATGCAAATTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGGACACCAGATCTAAGGAATTGTGACAGGGATCTCT
WI-21149a	167	G	A	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTTTAACAATGACCTTATTTATTTAACTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTACAC[G/A]TGCTTCAGAATGCGGCCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGAATGGAACCCCAGGCTCTACCTG
WI-21376b	188	A	G	---	GGTGTCAACTTGGAAATAATGGTTAAAAACAGGATAAGCATTAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTATCCCGCAAGTGGAGTTCATGTCCTGGTGAAACCA GACAGTGTGAATCGTGTTCCAGCCCAAATCTGCAGCCCCAAATCTGCATGGGGACTCTGGGGAGAGAGCCT GAACTGAGCACGCACTCATGTCTGTCGCATGGGGAACTCTGGGGAGAGAGCCT
WI-21382d	125	C	G	---	CCATTGCAGTCCAGAGATGAGAAACTGACCAGAGGCAAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTTCTAAGGATGGGAAGAGTGGGGGCGGGTTTGGATCCAGTCAGTGGGATNTGGCTTCCC[C/G]AGGTT GCAACCCAAGGAAGTCTCTGGAAGCAGCACCAGTGCTGCTGCTGTCGCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGTCCGAGGAGTCCGAGGAGAGCTCCGCAC
WI-21437a	201	G	A	---	TCCCTGAGGTTGGAGTCCTAGCATAGCTCCCCTCCCCTCAAAAGAGGGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGTGGGGCAGGAACATGCCAGGGCTGCTGGTAAATGCCAGGGGTCACCTTTACCAGGGGC[G /A]CAGGCATAGTGTGCCCCTGNCTGCCCCTGGGGGGAACACAGT
WI-21202b	156	A	C	---	CAAAATAGAAATTCTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTTAAGTTAACTGATTTATTATTGAGGG AGGAGGAGAGAGAGTTGACCAAAGTTCTACATGCATAGACACAGTCTATCTCAAACATG A
WI-21202a	61	T	C	---	CAAAATAGAAATTCTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATG[T/C]TGA TCTGTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTTAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGAGTTGACCAAAGTTCTACATGCATAGACACAGTCTATCTCAAACATG A

ID	Pos			Sequence
WI-21627b	153	A	G	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTGTATGATCAGCTCAGTTCCAGTATCCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAACAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGGGACAGTATACTACTCTACAATAAATAAGGTTTAAAAATGTGTTGCTTA
WI-21627a	106	A	G	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTGTATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGACAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGGGACAGTATACTACTCTACAATAAATAAGGTTTAAAAATGTGTTGCTTA
WI-21399a	75	C	T	GGATTTGAGTCCCAACTTGATCTCAAATTCACTTCTTGCATGTAAACAAGCTCATTCCCTCTAAAGTTTCAGTTT[C/T]TTCACCAGTAAAGGAAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAACTGCCCTTCTGCATTTGTCTCTGAGGTTGTGTGCCTAGGACTAGGTAGGATCTCTCTTGCTTCTGCCTTACCTAGGCATAGTGCCTGATAGCAGCAGGCCCAATTCATACTTGT
WI-20329a	68	G	A	CGATGTCTGCTAAGATAGGAGGTTAATTCTTTACATGGTGAGTGGGTCACAGAGACAAGAGACATCAATC[G/A]TCTGTTAGCAGCGGAGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGACAGCAGTGCTGGCTTCTTAAAAACAGTAAAACCAATCAAAAGAAAAGATTTAGAGGTTCAGACATTAGGAACAAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAAGGCCTCACT
WI-21249	155	T	C	TTCTGGCATTCAAATGTACATGTAAAATCCAATTTAACAGATCAAAATTGTTACACTAAGTTTCACTTAGTATCTAAGTATCCAATCACAATTGTATCCAAGTTCACTTTAAGGAAAACATTATAAAGGTAATTAAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTTATTTCCNATTTAACTACTGTTCATTGCGTAAAGTATGTTGTCCCAATTTCAGCTGTTTCAGCTGTTTTAAGGAATTATAAAACATTGAGA
WI-21504	147	C	T	TGACACAGCATCAATTTCATGATGAATACTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTTGGGTCATTTGAGAAAACATTTTCAGCACAATTACAGTGGGGGCACGGGCGTTCGGCTCCAGCTGGGTTTCCCAGATGCAACAAT[C/T]GCGGTTCTGCGGCTTCAGGAATTATAAAACCCTTCCACCTGGCCATGGTGGTGGTGTTCTCTATGGACCGAGGCCCTGAAACGCGGGGAGCAGGGGGCAGGGGGCAGAGGG... CAGGG
WI-21242	115	G	A	CTGCACCAGGAGGAGGACAGCTGCTGGCAGGGACTAATAAACCCTTCCACCTGGCCATGGTGGTGGTGTTCTCTATGGACCGAGGCCCTGAAACGCGGGGAGCAGGGGGCAGGGGGCAGGAGAAC[G/A]CACTAGCTTGGGGGGTGGGCACCAGCTTCAGACCCCTT
WI-21475c	181	A	G	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGGTGGCCTGATGTTGCCAGGAGTAGGATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCCAGCCTTCTCACTTGCTTACTAAGCACAGCAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTTGGAGAAGGCA[A/G]AAAAGCCACAGCAGCAACACTTAGGAGCAAGACACCCTTCCCGTTCCTCCACCTATTTCCTCCCCTGAAG

ID	Pos				Sequence
WI-21475b	117	A	T	---	TAGCCCTTCTGCCAACATCTGCCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGCAGTGCGTCTTCCACCCTATTCTCCACCCTGAAG ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTCTCCCCTGAAG
WI-20893d	207	A	G	---	TGTTTGTTGTTCCAGCCACCACATCTTCTCCAAAGGAACCCACCCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCATTTTTCTCTCTTTTACAATGCAGT TTC[A/G]ACATAACATTGGTAGAGTAAACAAACCACAAGCCTAAATG
WI-20893c	179	T	C	---	TGTTTGTTGTTCCAGCCACCATCTTCTCCAAAGGAACCCACCCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCAT[T/C]TTCTTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAAACCACAAGCCTAAATG
WI-19941c	71	C	G	---	GAGCTCAAGGGAAGACCCTTACCCAGATAGGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT[C/G]GGTCCTGGTGAGACAAAAGCAGGGGGCCTGAGAACACAGAGCAAGGTGGGTTTGGAG GGAGCACAGCAGGGTGCAGGAAGGGAGATGGGGGACCATTCCTATTCCAGTGCATGTCCCCTTAAAT AAACTGGGTACAGGAGCATTNTGGAAGGAGAACCAAGGACAAGAGAAGACAAAGCG
WI-21552b	166	C	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTAAATTAATTATTGAATTTAGTTACCCC ATTGTGCTATCAAATATTCAATCTTATTCATTCTTGTAACTATTATTTATTTGTA
WI-21552a	66	G	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /A]TAATAATTACTTCAGAAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAAATTAATTATTGAATTTAGTTACCCCA TTGTGCTATCAAATATTCAATCTTATTCATTCTTGTAACTATTATTTATTTGTA
WI-21512	54	C	G	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGCTGCTCTGGAGGCAACGTCCAGGTCGGGGAAAGGCACTCGTGGTCTGTGATCGTGTC TCAGTCGATGGGGAGGCTGCGTCGTCGTGGGGGTCCCCACAGCGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGCGTCGTCGTGGGGGTGCCTGGGGGG
WI-21513b	192	G	A	---	CACATAGTTTCTCAAGAAGAGGATGAACTGAAAACTCCTCTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAATCTTTAATTTATATTCTCCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG TATTCTCTACATACCACAGTATACACAACAATGATGGCCTTCCTGCAGGTTTAGGAAC

WI-21514b	133	C	T	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGACCTCAGAAAGCATTTGATTGTCAAGGGTCATAAGGAACT ANTTTAAGGCTCAGATGGGTTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A	G	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCA[A/G]TTCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	C	G	ATGAAACATGTTGCAGTGCGGATGAATT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	TTCATCGGTTCTTAATACAGTACAAATCCTTTGTTGAACAAAAGTCACACTGCAATGATTATTTACA GATCCAAAAATAGACTCAGGCTTCAGACATAAAATTAACATTC[A/G]TTCTAGTTCAGTGATTAGT CACAGAGAANTTAAACATCTGCCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141	A	C	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACTTGGAAGTGACTACACATGGCAATA AGCAGCCTATCTCTTACCAACCAGGAAGAAGTTCTTGGGGCATGGCATGGTGATGGTAGGCCCAGAGGC GGGAATA[A/C]TTACTACACTAAGCCTACACTGTTGTTCACTGTTCAGANTTCTAAGGCCCAGCAT AGTGGGAGGAAATGTGATGACTTCACTGTGTTGATTATGATGGAAGCAACTTATGAGTG
WI-21574a	235	C	T	AAACCCAGAATTTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAAATATTTGATCTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACTTACTGCCTCACTCCT[C/T]GTCTGTCAGGTGGGA
WI-21644c	151	T	A	TGACTGCCAAGAGATTTAGGCCCCAACTTAGGAGCAAGGGTCACCTCTAACCTTCAGGAAGTCTTGGGT GTGACCCACTGCTGCATAAATGGATTTCACCATANTATTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAACATGTGTTCTCAGC TTGGCCTACTGACCACCTTTCCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	G	A	TGTCTTTAACCTCCAAAAGTCCAAATAAAACATATAGACATTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCACTGTTGCAATTGCAATTTCAGTCACCTAAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGTGTGGGTTGTTGGGACTGGAACATTAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGTGG
WI-21615b	151	C	T	GACCGAGAAAAAACTGCAAGGCATATGATGTTTGTCGAAGTATCACATGATGATGAGTATCACTGACTATTTCAAGCTTATAGA GAAAACTTGCAAAAAAGTACAAAGATGGCTATTTTTAAATTTCATACATATTAAGATAAGGATGGACT CTTTCACTGAGTATTATC[C/T]AGGACACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCCCC TATTCTATATTGGGCCAAAGGGAAAAGGTAGGAAACGGAA

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WI-21981	61	T	A	---	TGTCATCTCATTCTGGAGAATCATAGAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT[T/A]GT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGAATTACAGGAACATGACAACATGCATGGGATAGA CACTCGTTCTCTCTACAGATCCGTGCTTGGGAATTCTAGTTGTAGGCGTTTAAGGTTAAATTTGG ATTACTTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120	C	T	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAAACAGATAGAACGGTGTAACACGCCTCTCCACTGCT TACTGTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAAGCCTAACCTGGCC[C/T]TGTCTTTTCAG GCTTCTCAGGATGCCCACAGCACATACTGGGGACTGGGATGCAGGGAGAAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211	C	T	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGTCCATGTGGTTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTCATCTTTGCGTCATAGACACGGGTGAGCTGAGCTCATGGTGGAACTCCTT GTCTGTAGGTTTCCAGGGGCAGGATTTCCACCCAGGGCCCAGGGTGCCCG ACAACTTC[C/T]TTCCAGGGGCAGGATTTCCACCCAGGGCCCAGGGTGCCCG
WI-19105a	33	T	C	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTT[T/C]GTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTCATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTTGTCTGTAGGTTTCCAGGGCTGGGCACAGATTTCCACCCAGGGCCCAGGGTGCCCG CCCACAACTTCCTCTCCAGGGGCAGGATTTCCACCCAGGGCCCAGGGTGCCCG
WI-21760c	81	C	A	---	CAAACCTAGTCACTCTACTGATGCAAATGATTGGAGAGGTGTCTTCCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGTCTCTCAGTTCAGGGCA
WI-21760a	35	A	G	---	CAAACCTAGTCACTCTACTGATGCAAATGATTGG[A/G]GGTGTCTTCCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCTCAGTTCAGGGCA
WI-21569b	198	T	C	---	TCTGCCCATATGTTCCCAGCACCACTATTACTGTTATATTCTCTTGAGGAAAACCAGGNATTAAG AAATCTGGTTTGAATTCCATGATGCTAACTCTATGGTTAAAAATCCTTTCCTTACCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTACT[T/C] AGAGACAATTCATAGTTCATAATCTTCAGGGTTGTGCTTACTTGGGGGGC
WI-20934a	72	T	G	---	CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAACAAATGGTCAAATATTCAAATGGCCTGGCACTAGTGGTAATTCCAGCAGAC AAACAGCATGAGAAAAAGGCCGGGAGACATTAGAAGAGACCCTNTTCCCCAGGAGA AAGCCCTTTACCTCCTTAAGATGGCAGATTAGAAGAGACCCTNTTCCCCAGGAGA
WI-21561	55	T	G	---	TTTCCATTTTATTCAGCGCGGCCATCAGAACAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAAC CTCTCCCAGGCAAAGAAGCAAAGAAAAAGTGATCATCTATTGAATTCCTCAGAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAAATATAATGATGATAAATGATAAATGTTCTGGA AATAATTTTTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA

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WI-21961c	200	T	G	---	AGCTTTGCTTGCTTACTTACTACTACCTTTGCAATTCTCTTATTATTATTATTACTTTTATTTTTCCGTAAGTTATTGGGGTACAGGAGGTATTTGGTTATATAAGTTCTTAGTGGCGATTTGTGTGATTTTGGTGCACCCATTACCCAAGTCCCAAAAGTCCGGTCTCTTTTATCCCTCGCCCC[t/G]cTCCCACTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTATGC
WI-21961b	73	G	A	---	AGCTTTGCTTGAAAATTTGGTACTTACTACTACCTTTGCAATTCTCTTATTATTATTATTACTTTTATTTTCC[G/A]TAAGTTATTGGGGTACAGGAGGTATTTGGTTATATAAGTTCTTAGTGGCGATTTGTGTGATTTTGGTGCACCCATTACCCAAGTCCCAAAAGTCCATTGTATCATTCTATGC
WI-21956	26	T	G	---	CCCACTTGGGTCTCTTTCAAGTGAAT[T/G]TTCCTTTCGTTCCTTCCGTTCCTGTTTCTGCTTCATGCCCCTCAGTCGAATTCTTCTTCCATTCCTGTTCTGAAACTTGCCTTAGTCTGTTTTCTGCTTCATGCCCCTCAGTCGAATTCTTCTCTGAGGCGGCAAGGACTGAAGTTGCTGTGGACCTGTCGTGTGGACCTGTCGTAGGGGTTACATTATGGGGTCAGGTTCTATCTCTTCCACCGGTAACAGAGAGGGGTTACATTATGGGGTCAGGTT
WI-21966	148	G	A	---	CAAACATACATTATGGCTGCCTTTATTTAAGAAAATGTTTACTGAGAATCTGTACTGTAACAACATATTTTTGTTAGAAGCATGAGTGAGTGTGTGTGTCGCGCGCCGCCGCGGCCACGGCATGGCACTGAGGGGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACTTGGTCGAAATCTTTGCTTATTAACCTTGGCCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146	G	C	---	TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCACCTGAGTAGTTGGTACATTGTACCCAACTTGTAGGCTTTATCCCTTACCCTACCTTCCACCCTCCCCCATTTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCTTGCATACCCATAGCTTAACTCCC
WI-21139a	165	T	C	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTACTACTAACTGCATGCATGCGACCTTGAGCAAGCCACTTAATTCTCTGCTCTCTGTGAAATGGGTACAATGTGGGTCAGTGAAAGGAACTAATAACAT[T/C]GTACAGCACTTCAGCACACAAGCCTGGGCACACAG
WI-20317b	217	G	T	---	CACTGCATGGAAATACACACAGGTAACATTTTAAACAGTGGGGACAAAATTTTAAGTACGTGGCCAGCTGTTGGTTGTCTTGTGTGTCAGTTTTTCATTATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGCTAGTGGTTACAAATTTGTTCTTCTTCAGTTTTTCATTATTAAATTAATTGCATATTTGAGGCTACTCTACCATCATCAGAAA[G/T]TATTATTAAATTAATTGCATATTTGAGGCTACTCT
WI-22082e	179	G	A	---	CAGGACTTGGTTTGCTTGCATAAGAAAATATGTCCCTTTTTGTTGAGTTATTGGTTGTGTGCGTTTTCCTTTTGCATAAGAAAATATGTCATTTAGTCCGAGGAGGCTCTTGCTTATCCGGATGACGGAGGGTACACGGGGCGGGTCCGCGTCCAGTTCCCGCCGAAGGACGTATTC[G/A]CTGAACTGGACGAGTCTACTCCTCCCCCACAGGAGCCCACGAGATTTCAAATCCTCTTGCTGCAACCTCT

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WI-22082b	67	C	T	CAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCCTTTTTGTTTGAGTTATTGGTTGTGTG[C/T]GTTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGGCGTCTTGCTTATCCGGATGACGGAGGGTACACGGGGCGTCCGCTCAGTTCCCGCCGAAGGACGTATTCGCTGAACTGGGACGAGTCTACTCCTCCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A	G	AACACAAACTCCATGCTTTTCAAGATTCCCACACCCAGATACTAAGACACATATTAAAATTTACAGCAATTAAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGAAAAAACCCTGGGCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACACAGTATTGCAGAATGGCTTCAGGATTAATTTGATTAATTTAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACACATCACC
WI-21723b	125	A	G	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTAGTCATATTCCCA[A/G]CAACAGCATGATAAAATAATTCAACTATGTAGAAATATGAAAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-21723a	82	G	A	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCAACAACAGCATGATAAAATAATTCAACTATGTAGAAATATGAAAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-22132	99	T	G	CAACAGATGCTTGAGCCAAAAAGCAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTCAACCTTTAATCTGACTTGCCTTTACTACTCCTT[T/G]CCCCATTCTTCCTCCTAATCTCTTTTGCCTTACAATATATTACCTCTAGGTATCACCTCATCCTATAGGAATGCCTTCTAGTTTAATGTCCTGCCCCAAACAATACTAACCCCATTGAAGGATAACTATGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A	G	TGACAGATCACCACCACATTTGTTTGTAACTTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAAGATTCTCTTAAAGAACAACACACACACGTGCACACAC[A/G]AGAGGCAAGTACAAAAATGTAACCCCACCAAAGTGCATGTGAATGCAAAAGCTTCATTGCAAACTCTGAGGATCATTCTCTCTGCTTCAGGAAATAAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C	G	CTGAGGCCTGCTCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCATTTTCTCTTTGTGTACAAAGGATTCAAAATATTTTCACATCTTCCTTCTGCTCAGTTAAAAACGTGCCGTGGCTC[G/A]CAATACACACCAAAGCCAAGGCGTAACTTGGCTGCCTCAGGAGGCTGGGAGGAGGTGCCAGATGGTA
WI-21079c	166	G	A	AATGAAAATGCCACCCAGAGGGTTAACAGCTTGCCATGCAACTGTGTGCGCAAAATCAAGTTGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAAGCTGTGTTGTTGCTCAACCCACTGACCATCTCAGCTCAAACTCAGGCCGATGACTATCACCTACACATCTGCCAGGGGTAATAGGCATGGGCAAAT

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WI-21079a	50	G	A	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCCAGCTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCACCCTGAAATATCTGCTAGTGGGGAATTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAAT
WI-22129a	45	T	G	TCTGTGTAGATTTTAGCCATGCCATATATTTAACTTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTCAAATATAAATAATTGGTTGCAAATTCCAGNAAAGGGCA TTAACCAAACATGGGACTGATCCTGGGGGCTTCCACCTGACTAAGGTTTA
WI-21941	79	A	G	TGGAGTTAAGTGGGGCTCTGTATTTCCCCAAGAAGGACTCGGAAGATGTTGATTCCAGGGCAGAGT GAGGGGCAGAC[A/G]GGATGAGGCTCTTCGTAAAGTCCAACACAGCGCTCACAGATGCTGGGAGGCT GGGGACTGCCAGGTTGGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCCACCACCACTCACC CAGCACACAGGCACACGCAGGGCACACACGNTGCACTCACCACGC
WI-18916b	42	C	T	AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCGCGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G	C	AATGGCATCCCTGTCGATACCAAACATCTTCAGCA[G/C]CTCAGCCGGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCGCGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A	G	TTCCCTTCTCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGCCAGGNCTTCTGGCCCCAATTCTGGGTTCTCCCCCAAG CCCATGCTTCTTCCTCACAATCTTTACTTCTTCCTCTGACCCTCACCACCACCAAAAT[A/G]CTTTTAATTCTGGAAAAGAAACCCAGCTGCACACTGGGGCACACTTGACCT
WI-21863b	47	C	T	CACAAGAGTCTGTACAACCTTAGGGACACCAGCCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCTC ATATCCCACCCCACCCCATCCCCGCCTCCTGCCCCAGACCCCCAGGCTCCCCTGCCTCTGCTGGTTGAAGTATTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCACAGCATCT
WI-19860	51	C	G	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCCAGTAT CTCCCCATCCCACATAATTTCTGTTTGATTTTGCCATTCACCCATAAAATGGTGGGATCTACCTCCCCT CCTTGCAAATTTGAGCTGGNCCTCTGTCTTCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C	T	ACCCAGCTCCTCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCATTTATTTCCCTCTTATTTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCTTGCCCACAGTCGTAACTATTGC

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WI-19891c	172	C	G	---	TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGTGCCCCTCCCCCCCGACTCCTCTGTCCTGGGAAACGTGGCTTTGNCTCCCAGACACGTTGTCAGATGCCAGCTCTCCTCAGCGGAGCTCCCGATCCCTCAATTGCCATCTGTCTGACTC[C/G]CGTCTTCCCGGGGCCGTGGGCGGCCGTTGCTTGTCAGGCAGGCGCGGGCGGGAGGAGGAGGAGGAGATCCAGGGTCTGTCTG
WI-20155a	81	C	T	---	GCACCTGTAGGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGCTGTACATTACCCTTAGGCTGACCATTCCCTTGCGGGGG[C/T]GCAAAACTGCTTGAGGAAATNTCCCCAGGAGGAATAAACTAGAAGACGCACCTGCTATTTCACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGAGTGCCCCAGGGTAAAAGTCTCTCTTCTGTCCAGTCCAGCAGAGACTTCTC
WI-20270b	91	T	G	---	AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAATACATTCATGTCCAGGATAAGGAGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCACGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCTGGGTGATCTTGTTCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGTGGGTGGGAA
WI-20270a	53	G	A	---	AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGC[G/A]TCAGTGTACAATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCACGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCTGGGTGATCTTGTTCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGTGGGTGGGAA
WI-20622	130	T	C	---	CCACTTTCAATATTTTACAAAATGCTCACGCAGCAAATATGAAAAGCTTCAACACTTTCCCTTTGTAACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTTCTGTATCTTAAAAGTTGAA[T/C]TACTAATTTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTGCCAATACATACATTATTTCTNTAACTTTATTTTACAATAAGCCAACATCTGTCATGCAG
WI-20768b	190	C	T	---	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCTAACAGGACCTCCTGCCTGCCTGCTCACGACTGATTACTTTCAATCCCAGCTGCAACTGAAACTCATTCTGTATCACCACTCTACAGGAGAGGTCTATTTCTGGGGCACCAGAAGNTCAGCACACATACTGCTGGGA[C/T]CAGGGACTCGTAATTCGGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-20768a	71	C	T	---	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCAGGCTAACAGGACCTCCTGCCTGCCTGCTCA[C/T]GACTGATTACTTTCAATCCCAGCTGCAACTGAAACTCATTCTGTATATCACCACTCTACAGGAGAGGTCTATTTCTGGGGCACCAGAAGNTCAGCACACATACTGCTGGGACTCAGGGACTCGTAATTCGGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-21909	153	A	T	---	TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTCTGTCACATCTAACGGCAACTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCATCTTTAAAGAAATGTCTTAACATACCAAAG[A/T]AGTGGAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTACGACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAAG

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WI-22202	128	A	G	TGTTGCTTGGTTGTTGTTGCTTTCTGGAAACATATTGGAAACACTTGTTTTCATAAGCTTGTGTCCTGACAGTGGCACAATCCCATCCATCTTCAGGCCTTTAATAAGGTCATTATGAAATCTGAATTTCTA[A/G]TTAATACTCTGGTGCATTCATTCATCTGCAAAGCAACTGGCACAACCACTCCTTGCCGGTGCAGCTCTCGGAGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70	C	T	CCAAGGATGAAATTCCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAAGTGTCCTATGAA[C/T]GAGGCGAGGAATGGGCATGCCGCTGCGGTACCAGCCTGGACGTTGCTTCCAAAGTACACTATGTGTGGTGGAGACAAAGGGT
WI-22283	109	T	C	GGGGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCGCCACTAACGAGCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTG[T/C]TTCATTTGCAAAATAAAACCCAGACCGGGTCATCTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCATGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136	C	T	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCTCTAAGCACCGGCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGGGGTCAGGACCTTGCTTT[C/T]TCCAATCTCTCCTTCTTAGCCAGAACTTGCGAGAGCCCCTTTNATTTCTCTCCCTCTATTCCCCTCCTTTCCCCAAATGTGCTAAGGTCCCAATTCCCAGACCCCTCCCAG
WI-22292	53	A	G	CCAGTTGGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTGCTCAGTACCAGA[A/G]GTTTGAGTACGGTCGTTTAAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186	C	T	ACCTTGCACACCTGCCATCCGGTGCCATCTCCTGCGTGCTGGCCACATCTATACCCACTCTGGCTCTGAAAGGCTTGTCACCAAAAATGGGCAGCTGGGCATATTTAAACAAAGGCTCCAAAGGACCCCTTTCACTTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAAGGCAGGATTGTGGT[C/T]CTTGTGTTTCTGAACAGGGCCCAGGGCAGGCAGCCAAGGCATGCCATCCATCCACTGCAGCACTCAACCCT
WI-22395b	127	A	G	GCCGTTCCAGTATTGATAATAATTTGTGTTTAATTTCTATACAGAATGGTTCTTTCTTGAATATTTTGTAGGGGATGGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTTAAT[A/G]AAGGAAATGTTACCAAATCCAATAGTGAAGAGTAGAAATATGTTCTTTAGAGTAGNTAGAAAGTCCCCAGGCTCCT
WI-22405	90	A	C	TTTATGGCTCCTGAGTGCCTTCACCCAGCTACACTTTACCTTGTATCTATAAAAGTGTAATTTAGAGTAAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAGCAAACAAAACTGCTGAAATGTGGCAAGGTTTCTCAGTG
WI-22419b	67	T	C	CCCTTCTGGACAGTTTGCTTATGTGTTCAGACAATCAAGGNTCGCCCTGAAGCATGGCGTGTGCACGAT/C]CTGGATGGCATCAGCAGGCTCCCCGGCCTTGAAGCACCCCATGGCCAGTGC[T
WI-21342d	59	T	C	ATTTTCCCTTCTGTGTTTCGTATTTCCCCTTTTGTCAGTAAATNAGCAATACACTGA[T/C]TGGAAATCTGCATGATTAAATAACATTAACAAGTTCATAAACACACCCATATAACACACCCCATATAAAGCAAGAAGAGGTTGAAAAATATCCCCTAACCGAATGCAAATTGCACATTCCCTCCTGAGTTT

ID	Pos			Sequence
WI-21763b	154	A	G	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACTGCTCTCCCAGCTGATT[A/G]CAGACATTGCCTGTGCTTCTACCCCAGCAGCTGTCTAGTGCACTTGA
WI-21763a	135	T	C	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCCCAGACTGTTCTCAGTCACTT[T/C]GCTCTCCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCCAGCAGCTGTCTAGTGCACTTGA
WI-22440	64	A	C	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCATTCTTCCTTATCTTGCTTAAGCCACTTGGGTA[A/C]TCCATTCCAGCTCTGCCACCTTCTCCAGTTTTCTCCATGTCAGAAGTCCCTGGGAGGGAGGGCTTTCTGGAAAT
WI-22449	74	T	C	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTATTAGCTGGCATCCGAATACAGTACTTCTTT[T/C]GAAAAAAATACACAATGGGAACTGACA
WI-21965a	112	A	G	CAGGTTCCACCAGAGCGTTTATTTCAGCCACTCAGGACCCTGGCTTTCTGCTCCAAGGCACTGAACACAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCCCACAGCC[A/G]CCCCCACCAGGGTTCTCTGTTTCCCAAGTCCTGATGGATTCAGGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGGTCATGAGGCAGCCAGCCTGTGGTGCCCAGCTCCAGTGTGCCAATGTGC
WI-21687c	115	C	G	CACCTGGCAGTTGAGTCAGATTGTGAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCAAACCACACATGTTCCTAGTCAGAAAGTCTTCATGGACTTTCCTCCTAAG[C/G]TGTTCTATGATCAGACCACCTCCTAAATGTGGCTTTTACCCATTACACAGGCTACACAGTTGAATCAGGCAGCAGCAGCTGCTGGAGAG
WI-22374a	149	T	C	AGCTTTTACAACAAAGCGAGGGTTAAGGAGCCTGAGGAAGAGAATTTCACAACTATTGACTATACAGAGTCTTCAATTCCAAAAACAGTTAATAGTAACTTGGTGGCACATACAAACATGCATTGAATACTCTGTATTATTCAGTAACTAAA[T/C]AGGNTCCTGCATCATTCTCTTCACA
WI-22250b	132	C	T	ACTTGTCTTCAGGCAGGCATTTCTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACTGTAGTGGGTTATTATGGGGTCTCTGCCTCCTGTGTTATG[C/T]GGANCCAGGAGGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G	A	ACTTGTCTTCAGGCAGGCATTTCTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGGTCTCTGGCTGTTATGCCGGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G	C	GCAGCCATCCTCCTCTCCAACACCTCCAACACTCCCAGGCCACCTCGGGCGCCCAGAGCCACCTCATGCCCAGCAGCACCTACGTGGCCCGAGTACGGACCCCGCCCTGGCCGCTCTCGGCGTTCTCAGCGACTCCCAGCCAAGTGGAGCCCCAGAGGGGCGGCGGCCGCGTGCTCGCAGGCGGGGACTCCCAGCCCAGAACCTG[G/C]AGTGCTTCTTTGACGGGGCGGCGCCGCCGTGCTCCTGGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C	T	---	GCAGCCATCCTCCTCTCCAACACCTCCAGGCCACCCTGGGGCCCAGAGAGCAACCTCATGCCCAGCAGCAC CTACGTGGCCCCGAGTACGGACCGACCCGCTGCCCAGGTTCTCGGCTTCTCAGGACGCCCAGCAAGTGGA GCCCAGAGGTTTG[C/T]TGGGACTCCAGCGCAGGGATGAGCCCAGGAGCCCAGAACCTGGAGTGCTTC TTTGACGGGGGCGGCGCGGTGCTCAGCTGCTCGGGAGGTGAGGAAGGAGGT
stFIBBb	412	G	C	---	GTGAGGAAGATGGACCTGGACAGAGACAGTCAGTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCGCATGAGCCCTTTGCCACGTGTCTGTTGTACACTTGCGCCCTCTCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTGTAGTGTAGCTTCCTTGAGAACCTTCCATGGTT AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stFIBBa	341	T	C	---	GTGAGGAAGATGGACCTGGACAGAGACAGTCAGTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCGCATGAGCCCTTTGCCACGTGTCTGTTGTACACTTGCGCCCTCTCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTGTAGTGTAGCTTCCTTGAGAACCTTCCATGGTT AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stIGLV2	61	T	C	---	GTCACAAGAGGGCAGCGCCTCTCGGGACGTCTCCACCATGGCCTGGGCTCTGCTGCTCCTCAC[T/C]CTC CTCACTCAGGACACACAGGTGACGCCCTCCAGGGAAGGGGTCTTGGGGACCTCTGGGCGTGATCCTTGGTC TCCTGTCTCCTCAGGCTCAGGGTCTCACTGGCATGT
stSG10017c	70	T	C	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGCGATCCTCCCACCTCCCAGGGTGCTGGGAT TA[T/C]AGGCATGAGCCCCACCACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG10017a	33	G	A	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGC[G/A]ATCCTCCCACCTCCCAGGGTGCTGG GATTATAGGCATGAGCCCCACCACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG10023	63	A	T	---	TAATGATAATTAGGGCATTCTTCCCACACGAAGATGACACAAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGGCTGTTTTTCCAGTAGTATGACAGTGA
stSG10096	36	G	C	---	GTGGAGAAAGATCGTCTTTCCTCCTCCTCCCATGACC[G/C]GGCTTCCCGCGGGCACCTGTGCGTTTTCC ACCCCGAGACGGCCCTTTGTAGGGGACCCACTCGCCCACTCCGGTTCGCGCCTCCTAG GGCTCGAGTGTTTAAG
stSG10118	107	C	A	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCAAGTCAAAGATGCCCCATTCCTTGCG[C/A]CTCAGCCCTCAGTTCCTTCATTCC ACCAGGCCGTGCCCTTGTTTGAGTTTTTCCTCCCCAGTGAG
stSG10120	89	T	C	---	TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTCAGACTATGC CGTGTTCACGGAACACTTTAATA[T/C]GTTGTTGTAATCTGATTTTATCCTCGTCTTACAAATG
stSG10178	42	C	T	---	TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAGTCCG[C/T]GGGAGGGAAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCCCTTAGTTAGGAGGATGTTAAAATACTTGGC

Name	Pos.			Sequence
stSG1019 3	136	G	A	GGAACAATACTACCTAAGGACAAAATACTATTATTAAAAAAAAGTCTTCTAGTGTATATTGTGTAACACATTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTGAGTCCATCTATACAAACTTTTACTT[G/A]TTGAAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143	G	T	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGTCTTCCGAGGGAAGCTCAGTCCTGGCCTTGCGAGAGTCAGCCCTTGGTCACCTCATAACGGGGCTCCAAGCTAAGGCGTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA[G/T]CAAGACCACAAGGCCAGATGCCCACTCCTCTTTGTTCTTACTTTCT
stSG1020 9b	75	A	G	TCTTTTCTCTTTCACTCTCAGTCACCATGTAATTATCAGCTGCTGAATTTTTTA[A/G]C[TCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34	C	T	TCTTTTCTCTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29	T	C	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAAGCCAGTTATTCTGA
stSG1025 2	108	A	C	ATAGGTTTCAGGAACAAAATCATTAAATGGAAAAATGAGAAGAATTCTTTATTTTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTCTTCCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTCAGAAATTCTCTCTTG
EST109150	123	A	C	CTGTATTAATTAAGAAGGCACTATTAATGAGGGACGGAAAAATCTACCTGTACACAAAATTCTGTACTTTAACAGCATCTTCAAATAAACCTTTAAAGGATAAATGGTTTACGATCATTTAAG[A/C]ATTTAAGAACTGAGTTATTTGGAC
EST110231	166	T	A	TTTTTGTTAAACCAACCACCCTGAAAGTTTCCACATGTGAAATATCAACAGTGAACAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACCAGTATCCTATCACCAGTAAACAGCAGGGCAATTAGTCAATTAAAAAAATAGTACATGTTAT[T/A]GTGTAATAAAATTACAAGGCTTTCCACTCGTGGATTGATTCCTTTTTTTGGAGGGAGGGAGTAATCCTGG
EST140968	71	G	C	GGGGATGTATATTACAGATAACACAACTCACAACAATATACCATCAGAACATTGAAAACTAAGGCCATTCTGTGA[G/C]TTATTTTAAAACTTGGTGTTTTGCACATAATGATCTTAAAAAAAATGAATTACCAAAACCAAGATTCTCTTCTAAAAATTAATGCAGGTACAGGATAACTTAGGGCTATATCTAATCTGAAG
EST221136c	125	C	A	TGCAAATTGTGAGAAGGCAGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTCGCAGGGATGCTTAAGTCTTAAGTCCTCTGGCAGAGACCCGAGGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTCTCTCAGGGTCGTGGAG
EST225557	60	G	A	TCAAGCATGTGTAAGGCACTGCCCCGCCAGACCCTTCTCAACTTCTGCACACTGGAAGGT[G/A]AAACCTGGGAGGAGAGAGACACTCCCCTCCCCTAGCTTCTACCTGGGCACCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAGGACAAAAGACCAGGGCTCAGAG

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EST22917-6	74	C	T	GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCAATAGAAA[C/T]TGACATGGGGCCAAAAGACTTCCCAGACAAAGCACGCGAAGGGTAGAGGATATAGGTTAGCATCATCTGGTTGTGA
EST36458-6	65	A	G	CAAGTTAGAACCATGCATCAGCTTTCATCCATGGTGTAACTTAACCCTCAGGCTGTCCTACTCA[A/G][T/G]TGGTTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745-3	56	A	G	GAGGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGCAAAAGTC[A/G]CTATGGGGCCAGACTGAGGTTGGACCACACAAGCACTCCAACGCGTGGTGAAGCCGCACAGCACGGAGTAGCCAT
STS-R37410c	201	A	T	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAAATCCTCACTTAAAAAAACAAAAAAACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGAATTTATGGTTTGAATAAAATACAAAATGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG[A/T]TATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410b	139	G	T	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAAATCCTCACTTAAAAAAACAAAAAAACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTAT[G/T]GTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTCTGGTATGATGTATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410a	48	C	T	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAAATCCTCA[C/T]TTAAAAAAACAAAAAAACCTTTGCAATGCTATCATTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTATAAACATTCTGGTGGAATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTCTGGTATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R42778	74	C	T	TATCGTGGAAGTTCCAACCTCATACTTATGCTGCTTTCTACTTGCTAATATTGGATGCTTCTTGCCAGGCTCTC[C/T]TTAAATTGTGCTGTAACCTGGGAAGAAACCTTCCTACTCTCCACAAACCCTGAA
UTR-04350	125	C	G	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCGTGTGGGGAGGTGGGACTGAGGAGCGACTGCTAATCAGTATGGGGTTTCCTCCCGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGAAGGTAGCACGACACTGTGAGTGCACTAA
stSG10266	55	T	C	GAAATAAACTAAAACTGCAAAGCAAATCACTGTTAATAAGAATTGTTCTTCTGT[T/C]GACAGTTGAAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCCTCAGAATGCGGGCAAACTCCTCTGTGAAAATGTAT
stSG10282	70	T	G	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCAATACTATCATTTATGAAATCTTTACAAGA[T/G]AAGCACAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG10310	128	C	A	CACTTTAGATATGAGGAAATGGTTTAATGGACACAAGGAGTCAGCCACGTTGGAACCAACATAGTTTCATACCACGTTGAAACCATGTGTTTGTATGCAAATAACAGCAAATAATTTTCACT[C/A]TTGTCAATGCCAATGCATTGATTGAGATTCAATTGCAGAAAGGCCCAGAAAAATGAGAAAGGATAACAAACTTTTGATAAAAGGTAAGAATTTCTGTGTG

ID	Pos				Sequence
stSG1033 1b	116	T	C	---	TTTAAAGCTACACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAAGGATGCATTTCGG GCTCCAACCTGTCCTAGGAAGGCCTAGACCTCAAACACCAACACCTCCA[T/C]GCATTTCCTCTCTTGG CTACTATGTCTCTTTCCCTGACTTCTGCCCTCTCCAGCTCTTGGGCTTCCCACCTGTTCCATCTGA CTTAGGACCCTCC
stSG1033 1a	107	A	T	---	TTTAAAGCTACACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAAGGATGCATTTCGG GCTCCAACCTGTCCTAGGAAGGCCTAGACCTCAAACACCA[A/T]CACCTCCATGCTGCTCCTCTCTTGG CTACTATGTCTCTTTCCCTGACTTCTGCCCTCTCCAGCTCTTGGGCTTCCCACCTGTTCCATCTGA CTTAGGACCCTCC
stSG1243 b	225	G	A	---	ATTGGCAAATGGGAAATGACACCAATCATTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAAATTATGTTCAGGCCCAGCATGGTAGCTTATGCCTGCAATCCCAGCACTTCGGGAGGCCAAGGAGA AGGATGCGCTTGAGCCAGGAGTTCGACACCGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAAGAAATTCTGTTC[G/A]AAAGTATTTCAGACCCAAAAGGAGGT
stSG1345 b	60	G	A	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACTAGTTTGCTTCTTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 a	54	T	G	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACTAGTTTGCTT[T/G]CTTACGCGCT TCACATTTAGCATGGGCCAAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1385 b	117	T	G	---	TTAATGTCATCCAGGGACGAGGGGCCAGGGATGGAGGGGCGAGGGGTTGAGGAGCGAGAGGCAGTTATTTT TGGGTGGGATTCACCACTCTTTTGTCAATGAAGAGGAGGGAGACTTGGTATTTTG[T/G]TCAATCATTAAGAA GACAAAGGGTTGTTGAACTTGACCTCGGGGGGGGGGATAGACATGGTATGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG
stSG139	69	T	C	---	TCGTCTCCTTTCCAGTCGTCTTCTGCCAGAAGCATCCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT [T/C]GCTTTGAGCACTCTGGCTGCCACTCTGGCTGCCACTGTGTACTGTCTTGCTGCCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCAGGCTCTCGTTGTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTGGCTTCCTCTCCATG[T/C]AGTCTCTCCATGTGCAAACAAGATGGC TACTGGTGGTCCCAGGTTCCAGGTTCACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA AGTCCATAACTCAATCCTTGGGAAG
stSG1427	103	T	C	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTTGTAGGTCC[A/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCTTCCTATCCTACC GCA
stSG1471	50	A	G	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTTAGTCTAAG[T/C]TTAATTCAAAGGTTGAGA ATGACGAATTCAAGAAATTCTTCATACATAAATTGCTTTCCTTAGTTCTGCAGATGGGTA
stSG1483	44	T	C	---	CACACCCACCAAGTTTCATGTCAATGCCAAGTATCAAACTCTTGAGGACAAAGGCAAAACCAGTGTGCA [C/G]AATGTGGGAGGATGTCTGTTGCAGCTGAGTAGTTACTAATGCAGGAAAACCCAATGCAAAGAGGAA
stSG1696	67	C	G	---	AATGCCCTGA

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stSG1847 b	95	G	A	---	TTGCAGACAACAAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACCCCTAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAATGTGTGAAAAAATAACTTGATCACTGTGCT TCAAACACAACTG
stSG1847 a	49	C	A	---	TTGCAGACAACAAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCAATGTGTGAAAAAATAACTTGATCACTGTGC TTCAAACACAACTG
stSG1897 a	83	A	G	---	CTTAATGCGCCCTTCCTCCTTCCTTCTGCACAGGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[A/G]GCCCACCACCTTCTCCCGGTCCTCCCAAGATGACT
stSG2022 a	86	T	C	---	TGTCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTTAACATTAATATACA[T/C]ATTCCATAATCTCATCTATTAACATTAACACAGGCCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTCCTGACTCTGTAGGGACAGTGGGCCTCAGTTGGGGGGTTGAC T
stSG2076	104	C	G	---	AAACGTTGTCCCAAAATTGTGTTCAGTTCACAAGTATAAAATAGAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGCATTT
stSG2108 c	71	A	G	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAATGATTGAGGGGCTCCACAGAGA GAGC[A/G]TTAAGGGGAAGACTTTATAGGACAACTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2108 a	49	T	C	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAATGATT[C/C]GAGGGGCTCCACAG AGAGAGCAGCATAAGGGGAAGACTTTATAGGACAACTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2141 b	173	A	G	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGGCATGGCATGGTGGTGCAGGTGGGT GCAGTTCCCTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTTGCTCTG
stSG2141 a	113	C	T	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTTGCTCTG

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stSG22148	50	A	G	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTC[A/G]AAAGAAACAATAAATGTGGATTAGAAAGGAAACATCCATTACTGTATTTCGATACTTGTGATGTTCCACAGACGAGCTCATCAC
stSG2175	68	C	T	---	CTCAATGAGGACTCCATCAGCCAAGCCAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT[C/T]GCCGGCGGTGACTCAGCTAATGCTACCGGGGTTGGAGCGCCACCGAGCCCAGCCCACCTTTTCCATACCTGGGCAGAGGGAAGGGAGTGGAAGGACCA
stSG2189	41	C	T	---	CAAGTGGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACACATTCCCTCCAGTATAATAGGAACTCATCGCTAACTTTGAGCACTTAGTGTTCTGGTACTTCGTATAGGTTATCTCAATCCTACTCCAGCTTTGCGAAC
stSG2200	49	T	C	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTATAATGTCTTACCTGATGATCACCAACATATTACTACGCCTTATAGATGAGGATGGCAGCTTGGCTGGTCAAT
stSG2243	85	G	T	---	CATTTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAAGATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A	C	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/C]CTGTCAGGAACTCTCGCCAAGCACTGGGCTGCTGTCCTCAGGCAGAATTCTTCCT
stSG2306	67	A	G	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAAACAGTAGCTATATGATATTTGGGAACTATTTTACA[A/G]TATGCTCCCATTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACTGTTTCACAGTTCCTCCAGAGA
stSG2334	70	T	G	---	GAAAACTACCCCACCAGCATCATGTTAAAAGAAGAGATGAAAGAAGAAAAATCCCGCAAAAAACAAAAA[T/G]TGCAGTGGAGGGGCGTGTGGGAGGGGTGAATG
stSG2339	63	T	C	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTGTCTTGACTGCAGAAGTAACTGCTGTCAC[T/C]GTTCTCAGAGTCACCATTACGGTGACTGTGTCTATTCTGTGCTTCTATTCATCA
stSG2465	76	C	T	---	CAAGACTAAGAAGCCGCACCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATGCAGAAACCA[C/T]TACAGATTAAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTCATCTTCAAAGTGTGGGGTATGCA
stSG2549	140	T	C	---	TTGCAGGCTTGTATTCCACAATAAACAAAGTCATTGTATAGAGAATGTGAAAATGATACTTGAAAACCAAGATATATAAAAATATTGAAGTCATTTATGCCTTTTGATGACTGGGTTAAAAATGCAAGCAGCTAAAGGAATATT[T/C]TACACCACCCACCCCTTTTTAACT
stSG2577	123	T	G	---	AATTGCCAAATGGAAAATTCCCAGAGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATCCCGGCCCCAGATTAATTATT
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stSG2577 a	121	C	T	---	AATTGCCAAATGAAAATTCCCAGAGAGGATTTTAGACCAACTTTGCCCTGTTGCCTTCCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCCAGATTAATTATT
stSG2700	58	G	A	---	ATCTCCTCGACTGCTTAGTGGGGAAAGGAATCAATTATTTATGAACTGTCCGGCCCC[G/A]AGTCAC TCAGCGGTTTGCGGGAAAATAAACCACTGGTCCCAGAGCAGGAAGGCTACTTGAGCCGGACACCA
stSG2724 b	101	T	G	---	AAACAAGCTTTGTCATTTCCACTACATTTTGTTGTGCTTTATATTTAATATTTGCAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTTTTTAATCCTGGGGTGTTGAAAGAAC
stSG2776 a	65	G	A	---	GTGGCCGATCTTTACTTTTCCCAGAAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TTATTGGCCCTTTGGAGTTAGGCCCAGGAACTTCAAACAAGGGACACTGCTGGCCAACCACAAAA ATATCCACTAATTCCCGAATATAGTAACCCTGTCTTGTCCGAATG
stSG2791 b	109	G	T	---	AAGGAAAGGTGGAGGGAAGAAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTAATAAATATT[G/T]GGGTCCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100	A	G	---	AAGGAAAGGTGGAGGGAAGAAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTA[A/G]TAAATATTGGGGTCCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85	C	T	---	CCGCAATTTTCAACACACATTCTATGAAAACTAAGGGTGGATCATGTACAAACACAAAAAACAAGC TCCCTCCCTCCAAAACAAA[C/T]GAAACAAAATAAAGAAAGAAATAAAATGCCCAGGTTTA ATTTTTTCC
stSG2850	88	G	A	---	ATGGGTGCATTGTAAAAGGCAAATTAAATACTTTTCAGGCAGGGCTGGCAAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGGCC[G/A]GGCTCACACATCCCATCAAATACTCCTCCCAT
stSG3031	71	T	C	---	ATACTCACGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCCTGGCATTTCTGTGGTGTCAGC AAA[T/C]GCCCCTTTATTTTAAATGATTCCAGACACATCTGGGCAGCATAGCT
stSG3058	81	G	A	---	GTCCCAACTCCTCTCCTCTTAGAGAAGAAGCATCAAAGGCAAAAACTGTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAAAGGCAAAAACTGGCTGAGGC
stSG3092	94	T	G	---	CAGCATCTTCCAGAACATTCCTAGAACTGAACCATTCTTGTCACTATTGAAAAACAAAGCCAAGTTC CAAATCCAAAATAATAAATGAACGTGC[T/G]GATAAACATTCTTCTTATGGTTCCAGCCCTACTTT AGTT
stSG3230	95	A	G	---	AAGAAGTACTTTGGTAGTAGCTATTTAAATAAGAGGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGTGCTAAGTGTTCTGAACTGAAGTAG
stSG3245	160	G	C	---	ACATCTCATACCCAGTAAGATCAAGAAAGGAATATCTGAGAGCAAGAATATCTGAGAGCAAGACGCCCTGCTCCAGGGGGCCC CAGGTATGTGTAGAGAGCCCAGTGGGGGTGGCCACTTGGTGTTTCTACCACCCCTGGTGTTCCATCCAGTCTG GCCCCAGTCGTACCTACCTGGGAGGTTG[G/C]TGTACTTGGCTACTTCATGCTTTAT

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stSG3265	42	T	C	---	AGGTGAAATGAGTTACTAAATGTAGCATTATTTATAAGGAA[T/C]CGCATTGTGTGAATAGTTTCTCAG TTTTCATTATGGAAAGATGATGATTTCAGCCCACATTCAGTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAAA ATCTGTCTGTCAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141	C	T	---	TGTACTTACTGTGTCATCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGGTCCTCCCAAAGTTACCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3269 a	24	A	G	---	TGTACTTACTGTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGGTCCTCCCAAAGTTACCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3284	130	C	T	---	TTAACTCAAGAACTTCAGTTACAGGAAGAGATTTATCTAATATTAAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAAATCCATATTAGCACTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTGATCTACCC
stSG3292	99	A	T	---	GTCTCAAGTGAATCTGTAAATACATTTTAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTTCCTAACTTCAA
stSG3323	26	C	A	---	TAAATGTCATATCTTAGCTCTCACT[C/A]CCAGTGTATCCATTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGCTTCATTCCTTTAA
stSG3369	69	C	T	---	GATCCCCAGTATTATTTCTAAATTGAACTTGTTTGTTGGAAATAAAAATCTGAGGACCACTCAGAG GG[C/T]TATAAGGGAACCCTCTTTGTCTTTAGTTCATAAGGACTTTCT
stSG3398	125	G	T	---	CAAGACTGTAAGAACGTAGGCCTTGTGAGAGTGAAGGAAGGATGCTGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC[G/T]CTGGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3416 a	43	A	G	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGAGACAAGTCACCATGCCTA CCTAAGTTTTTGTGAAGACAG
stSG3424	173	T	A	---	GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACTCCTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCCCCGGCCGACTTTTAAACTGAAT GTTGAAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCTTATCTGTAACAAAATGGACAAACAGAACTTTTCCTTCCTCTC
stSG3436	88	T	A	---	GTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAGGTGATGTGATGGGAGGCCTCACAGA ATGAGGTGGCAGAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTTCCTATC

stSG3463	103	C	T	---	GATACAGAAGAGATAGTGTGGTATGGATGGATAGTAGTATGAAGGACAAATAATACAAATATATTTTATTG AAATAAACAAAAAATGCATACACAGCTCAATGGGTCAC[C/T]TGGAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71	G	A	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGCTGGCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTACTGCACCTGTGGATTTCTTATTAAACTCATTTATACTATTTCTGTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C	T	---	TAGCCATCTTACTCTCTAGTTCTTTTGGGTTTA[C/T]GCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTATCTTTATCTTACTGGTCTC
stSG3536	213	A	G	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTAGCCTACTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGTACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTCACTGTGTTATATTGTTAAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGTGTTCTCAGTCCTTGCCATGAAGTATG
stSG3583	112	G	A	---	GAAAAAGCTTAACATACGATCCATGTGCAAACCCCAAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60	G	C	---	CCTAGTAACATAGTGAGACCTCGTCTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACTCCAGCCTGAGACTGTTTCAAAAA
stSG3589	101	T	C	---	ATATAGTAGTGCTGGTAGCATTATAAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCTGGCACAAAAACCCCAATGA[T/C]CCTATTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAAGCTATATACAC
stSG3590 a	70	A	T	---	GAGAGATGAGCTATTTATTCTTTTACTTAATGAAGATGTAAGAAAATGATCTTCTGTTCTAAAAAAAA AAA[A/T]TTTCTCTGATGTCTCTTGACCCTGTAGGAAACACATTCAGTTCTACACT
stSG3619	78	A	C	---	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40	T	C	---	ACATATGTAACTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]GGATTGAGAGGCATGAACCAAGG ATGGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70	G	A	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTGAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55	A G	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43	A T	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85	A C	---	ATTGTTTCCCTGAACATTCCCGTGCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCT GAAATATCCTACGGAGGC[A/C]TCGCCCCTCCGAGACTGACGATTATTAACCACCACGGAAAAAGG
stSG3693 a	30	C T	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCTGGACTCA CCTGAAATATCCTACGGAGGCATCGCCCCTCCGAGACTGACGATTATTAACCACCACGGAAAAAGG
stSG3698 b	145	G A	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51	C G	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAATAACCCACCTTCCCTCACTGCAGA
stSG3724	107	C T	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGCGAGCCATCCCTGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGCTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104	G A	---	GCCAAAACAAAAGATCTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACCAGCCAACAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G A	---	CGGAAGAAGAAACACAAATCCACAGAACAATCTATGGTTCATACCTTTTAGAAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTTGCAAGAG
stSG3787	49	T A	---	TTCTGTGCAAAAGAATCCACATCATTGTTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAAACCAAACAAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115	G C	---	GACAAGAGGGGAAGAGATGCGCCAGAGACCAGGGCTGGGGCTCGAGTGCCAGGCGC CACCACACGTCCTGTGGGTCAAGGCCCCTCCTCGGGAGCAGGTCTA[G/C]GCGGCCACGGAGGATGCAG GGCTGGGAGGGGAGGGGACCCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT

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stSG3880a	36	G	C	---	GACAAGAGAGGAAGAGAGATGCGCCAGAGACCAGGGGCTG[G/C]GGCCAGCTGGGGGTCCCTGAGTGCCAGGCGCCACCACAGTCCTGTGGGTCAAGGCCCCTCCTCTGGGGAGCCAGGTCTAGGGCCACGGAGGATGCCAGGGGCTGGGAGGGGGACCCCACCTCGGGGAACCCAAAAGGAGTCCATTTCTGCCCT
stSG3895	44	A	G	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTTGT[A/G]TTTTTTTCCATTAACTAATACATGCCCTCACAGATATATTCAATTAGTGTTATCACCATGGGAACAAGATGCTGATTCGTCAACTGAAAAT
stSG3902	104	T	C	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACATCATCTATTTCACCTAAATGTGAACTGCTTTCTTTC[T/C]TCJTCAGCTCAATAGCTTAACATCTAATTCATGTTTGCTCTCCCTTTGCTGGACAAT
stSG3935	50	G	A	---	GGGGTGTCTGACGGACAGGCACACCCAGTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGCTCCTCCCCCAGTTCCCACCAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40	25	A	G	---	GAGGAAGAGGTTGAAGAAGTGCTGA[A/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGCCCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGTATGTATCACCCAA
stSG4009	32	A	G	---	GTGTGGGCTGTCTGCTGATGATGAATGGCGCGCCTC[A/G]TACTCTTTACGGTCTTACACTTTTATGCTCCTATGAATTCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
stSG4033	123	T	C	---	AGAAGCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATTGAAACTACAGTGCAGTAACCAAAGAACCTAATGTTTCAAGCATAAAGGTACTTT[T/C]TGTGAACAGGTGGGCAACAC
stSG4038a	29	G	A	---	GCTGAGAGCACGTGTACAGCCACGCCACGCCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCCCATGTTCCTCAGTCGGTTCAGGCTCCCGGAGAGCACCTGAGGGTCCATCACT
stSG406	53	T	C	---	ACTGTGGTTCAACAGTATTGCGTTGTGTCAGACTAGGAGAAGCTAAACGAACAAAA[T/C]GGTTTTAGTTTTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAAGAGATTATTAACTTTTATCAGGTGTTAACATCTGTTTCAGGAACATGGCA
stSG4095b	55	G	T	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAAAGTTTGCTTCTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTGGAGAATCAAGCCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4095a	27	A	C	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAAGTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAGCCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G	A	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAAACTTACGTACTTATTACGTACTACTTATGGATAATCAC[G/A]CTTTTTCCCCTCAGAGCCCACAGTTAAACACGTTCCAGCACCATTAATCCACCGAGCT

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stSG4128	54	A	G	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT[A/G]TATATTATTT TACTTCTTCTGAAAATGCCACATAATTGCAATAAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G	A	---	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGGACCACGAGGCGACCAGGTGCTTTGATGCCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G	A	---	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGGACCACGAGGCGACCAGGTGCTTTGATGCCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G	A	---	CATTACCCAGAAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCCGGGACTCCCGCGATGGCTGGGGG GCTATGGCTCTGACAAGAGGATGAGCGGGGGCCGGGAGGCGGGGCAGGGCCAGACGTGAC TGGGGGGACCATGGCCGAAGAGAGGATGACCGGTCATG
stSG4301	81	T	G	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCCACACTTTCCAT TTAAGCAAATAAATT[T/G]AGCTTCTGAGTAGTTGTTCCCAGTTTCACCCAACATTTTG
stSG4331 b	71	T	G	---	CTCACAAAGGCCAACACAGAAAAAGATACAAAATACATTCATCCAGCTAATATTAGTTTTATGACAC AGAG[T/G]TTTCAAACAAGTTTAAGTGTCACCTGAAGAGCATGTTAAAAGTTAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTCTGTTTGAGGGGTGTGC
stSG4340	76	G	A	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109	A	C	---	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T	C	---	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	---	TTTCACTGCTACTGGTTTCGGTGTCTGGTGTGTCTGAGTCTTCGAGTGCTTGCAAGTGCTTCTCCAAGGGGAG AACAG[A/G]CTGGAACTGCGGGCTCTGCCATAGCCGGAATGACAACATACGATTTTCTT[T/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGTCTCCATGTCCATGTCCAGAACACCCATTAAATTCCATGCC
stSG4381	50	T	C	---	GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTTCTT[T/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGTCTCCATGTCCATGTCCAGAACACCCATTAAATTCCATGCC
stSG4410	79	A	G	---	ACCAAATGGTTCTGCTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAACACCGC[A/G]TGACAACGAACCCAGTGACTGTGAAACTCAGGCTGCGAGGAGGGTGGCTTGT CAGCTGGGT

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stSG443	65	C	T	---	AGCAGATCAGTCAGCCCACTTGTCTCTCTCTTCTTTAGGGAGGAGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGAGAAAATAACCAACTGGTAGGAGTGGGGAGGGGAGGGGGAGGGGAATAGGCAC AAATGGAATTCTATCCTGGCTGCTGTCCTTCTGCAGGTC
stSG4430 a	54	A	G	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT[A/G]ATTAACATA GGTAGGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGAGGGCCATTTT
stSG4448	99	G	A	---	CCTCCCTTCCCTTCCTTCCCTTCCATACTGTTCCCCTCCCGCCCCAGGCTCT CGCCTAGCCCTGCCCTCTGGGGTCACTGC[G/A]TGGGTTAGGCCCCCAAAAA
stSG4449	92	T	C	---	ATTAGCCATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGATGTTACAAT TAACTTTGGACAACTTAAACTTA[T/C]TAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA GGGCTGAACATAATTATTAAAAGAGCAAAGTTACCCCTCC
stSG4467	42	C	A	---	CAGACATGAGGGATGGCCCGTGTCTCTCTGGGACAGAGCCTCA[C/A]AGATGATGTCCATGTTTTGTGT GAATGAAACTCAAACACTCTTCAGTTTTTAGAGTCATTTCTGGTATCGAGCGACCACCGAGGAG CACACCCTGCTTCCAAGGCTGCTGCCCTTCTCGCACACAGT
stSG4475	21	A	C	---	ACATGTCATTTCCTGACCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA TTAAGAGACACAAACTGGACTTTGTTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A	G	---	GTAACATTCTGGGGGTGGGGGTGAGACAAAACA[A/G]ATGAACCAATAATTACAATTATACATT TCAAGGAGACTTTTAATCTAGGTAATGTGAAACGCAGCCATCAATGGTTTGTCAGGAAAAGGGAGA TGAAGTCTTGCTCTGGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C	T	---	TGAACTCAGAGCTGTGGGTGTGGGGAGCTGCAGCGGAGGGCTGGGGCGGCGCGGGGA CAGCAGGCCGGTCG[C/T]GCCACGTCGTCCTGGCCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGGATCT GATTCTCATTGACACGGGGAGACGGCTGTTGTTCATCAA
stSG4550 b	86	G	A	---	TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGCACC[G/A]ACAATTGGAGGGAAGGCGGGGGCAGGGTTTAGAGAAC
stSG4550 a	85	C	G	---	TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGCGCAC[C/G]GCAATTGGAGGGAAGGCGGGGGCAGGGTTTAGAGAAC
stSG4590	47	A	G	---	AATCAGGCACAAGCTCGGGAGAGAAGCCAACAAAAGCTCTTCTGCAC[A/G]ATGGGAGGGAGGACAC CATTGAAAAAGGCATCGTTCCTTCTTCATGCAAGCGAGGCCTGGCCTCCCACAGGCATGGTCTCCTTG
stSG4623	22	T	C	---	AATCTGTATCACCCAGCGCTGG[T/C]CAATGTACTCTAGTAGCTTTCCACAGGGATTTTTATACTATTC CTATAAGGTTTTATCATGAATAAAAAGCTCACAACTCTTTCAGCCATTGCAGATTCACATTTATCT TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A	C	---	TAAAAAAAAACAACCCCCCACAAAAAAACACCCAGAAGTTTTGAGTTTTATGTTTCAGATTTAAAG GTATTTTCTTTCTTAGCTTCTAAATTTTGAGTCATT[A/C]ATCAGAAAGTCTTCCCTACTCCAAGGTGA GAAAGGA

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stSG4850 a	38	C	T	...	GGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC[C/T]GTGCACTTGCAGGCCCACGTCAGGAG AGCCAGCGCGGTGCCCTGTCGCGGGAGGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86	A	G	...	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGGAGGGTGGTGGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G	A	...	ACTGGACTGCCTCGCTTGCTGAGCGCGGCTGGAGCGGGGCTGGGACTGCGGGCTGCGCTCTTCAG AGACTCGCGCCCGCCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGGACC
stSG4896	112	C	T	...	AAACAAATCAAACCCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCCTGCCATAGAGA GGTTGGGGGGCAGCTGAGGAGTGGTGGGGGCTGAGGAGTGGGGGCCACCTTTTCT[C/T]CAGCCACAGGCCCCTGAGG AATTAATTGACTG
stSG4932	22	G	A	...	ACAGTGCCGATGGTTACACAAT[G/A]TTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGGGTGCAGGGTGCTGGTTTCTGGTCCT
stSG4950	24	A	G	...	TCATGACTCCCAGGAAAAGGTCCT[A/G]TTAGCTTCCTCCTCCCTACTTCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136	G	A	...	AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGGCCCTGCTCTATTCAAC
stSG4961	91	C	T	...	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGTAGAAAGGAAAAGTA[C/T]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	A	G	...	ACTGGTGCCTCTCAGCAGATTCAGGGGTCGTGCAGGGGCTGGTTACCACAAACTCAGTAGGAGTGCAA GGGCT[A/G]TACCCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22	T	C	...	CAAAGGAGAGTAGGAGCCCCAA[T/C]TTTAATGGTTCCTCTCCCCCTCATGCTCATTTGATCCAAAAA CTATATACAATTTTGTAGCAGTCTCTGTATAGTTATTACACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAT
stSG6312	37	C	T	...	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCCTCCCCTGATGCATTGAAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G	A	...	GCTCTGGTCAAGCAAATTCTCCAGGACAGAAGCAACAAGGACAACAAGGACTAAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[G/A]ATAGTTCAGGCAATTAAGAATAT GCAACCCAGAGAATTCTGTGAAAACATTTTGCTCTTTGGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

ID	Pos				Sequence
stSG6362	88	G	C	---	TGTGAAATGTACACTCAGGTCTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAAGGAGGAGGAGGAACAGATCTGCACAGAAT
stSG8010	62	G	T	---	CACATCTGTGTTTCTGGAGCAAAGGGAAACCACAGAGAGGCCAGGAGTTGGGTGTGCACTGG[G/T]TGTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTGCTCCTGAGCGTGCAGAGAATAGATGGCTT
stSG8022	53	G	A	---	AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGGAGTTATTTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGAGGCAGGTTTATCAGCACACGCTGTATCTCC
stSG8032	67	G	C	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGTT[G/C]TGGGGAGGCAGGGTAGCAAGATAAAAAGAGGAGGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C	A	---	AGCTGGCTCTTCCTTCCTTGTCTGTGTTCGGGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCTGGGTGGCCTGCAGGACCAGGGGGTGGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8064 a	23	G	C	---	AGCTGGCTCTTCCTTCCTTGTCGCGT[G/C]TTCGGGGAGGCTTCACGTCCTCCGCCCCGTGGTCCTGGGTGGCCTGCAGGACCAGGGGGTGGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8072	59	A	G	---	CACCATCATCACATCGAGTAGGCTGAGGAGCAGGAGGGTGGGGTCTTGCTGTCTTCAGCCTGTCGTGTTCAAAAGAGGGCAGAAGGAGAAGTCCGAGTATTAGTGGCCGCATGGGACCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40	A	G	---	ATACACCCACACCACCCCACTCAACCTTGTATCAAATTCCA[A/G]AAGTGTAACTAAAGTATAAGAATATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAATTCAAGTTCAAGTATTATAACAAGTATCTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138	T	C	---	AAGGCTCCTTGAAAGCATGGTTTATTTGTTCCATTAACTTGTTCTCAGCTATACTGAAGTATGATTGACAAATAAAACTTGCATATATCATAATGTGAGTAGTACAGTGTGATGACATGTATATACAATGTGAAATGGTTTAGGAAATGTGATGGTTGA[T/C]TGTCATAATCATAATCAATAATTGGT
stSG8105	110	A	G	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCGTCTTGTGCTTGTTAATACACAGATGACTAGGCCCACCTGCGGGAGTTCCTGTTGGAGTCTAGGCCTGAGAATATTC[A/G]TTTCTAACAAGTTCCCAGGTGACCCTGAGGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96	T	C	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAATGACTGAGTGTCGCGTGGATGGTCGCCTGATGGTCCTGTCTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTCGCCTGAGCC[T/C]GTGCCCGTGTCTTCAGCAGCACAGTTCC
stSG8130 a	36	C	G	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAATGA[C/G]TGGATGGTCGCCTGCTTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTCGCCTGAGCCTGTGCTTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124	T	A	---	TTGTTGGACTTCAAATTCTTTCCTTCAGATTTTAAAATGACATTTATGCATGTACATATTTTAAAATTTAGAGAAACACAAATTGTGAACACAAATCTAAGAAATGAATGAAATGAGATGT[T/A]CTGAAAGTCTGATTCAAACACTTATCTTAAACTGACTTCTCAATCCTCTGTGTCCTCTGTGTGAAGG

Name					Sequence
stSG8145 a	97	C	T	...	TTGTGGACTTCAAATTCTTCCTTCAGATTTAAAATGACATTATGCATGTACATATTTTAAAATTT AGACACATTTAGAGAACACAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCGTCTCGTCTGTGTGAAGG
stSG8150	36	A	G	...	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGT[A/G]ATAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	C	T	...	AGAGGATTATGGAGAGAGCTGGGCAGGATC[C/T]CAACATTATGACCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAGAAAAAACGCTCATCAAAA
stSG8466	111	G	A	...	TGTGTATTGGGTGACTGTAGCCTAAGGATAAAATGAAATAAATGACACAATGTTATAAGCAGTGGGA GGAGTGAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--			...	GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCGTCTCCCGTCGGGGGCAACCCCGGCTTCCATGA GGCCATTGGGGACGTGCTGCCGCTCTCCACTCCTGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA	--			...	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCACTGTTCCTCTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGGCCAGAAGTGGACATGGACCTGTGAGGACTCCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
ESTD-AK-168	--			...	GGGGAGTGACAGCTAGAGCTAGCACCAAGGGGGCCTGTGTTTCTCATGGAGGACAGGCCTCTGCTC ATTCTGG
ESTD-ALB	--			...	AATCCCAGCACTTTAGGAGGCTGAGGCAGGCAGATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAAAAATTACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGAAGGTTGTTGGTGAGCCGAGAT GGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTC
ESTD-ANT1	--			...	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--			...	CCAGGTGTTGTGGCACGTGCCTGTAATCCCAGCTACTCGGGGAGGCTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGTTGCAGTGAGCTGAGATCATGCGCCACTGCACTCCAGCCTGGGCGACAGAGCAAG ACTCC
ESTD-ARSB	--			...	GGAAGAAAATGGAGCCTGTGTGGGAAGGAGGCCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCCACATCTCGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGACACCACCAATGCCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAAACCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCGTGCTGCATAAATATTGACCCAAAC

ESTD-AT3a	--	AGACCTCAGTTCCTCTCTTCTGTGTAAAAGGGAAGTTTGTTCTTGGATCTCCATGGCGGCCCAGCCAGCACTG GTGCCCCTGTGAGTCTGTATCCAGGTAGAGGATGGGACCAGGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGACAAAGAGACAGAATATTAAGAGAGCTGGGGAAATGTGG
ESTD-B3AR	--	GGCTGCCAGGGGTTCCGTGGGAGCGGCGGCCCTAGCCGGCGGCCCTGCTGCGGCGGCCGGTGCTGGCCACC GTGGGGAGGCAACCTGCTGGGGGCCCCGACTCCGCCATCGTGGCCATCGTGGCCGCTGGTGCTGGCCAACGT GTTCGTGTGACTTCGCTGCCGCTGGCCCGAGCCGACCTGGTGATGGCACTCCTGGTGGTGCCGCGGCCCACCTT GGCGC
ESTD-BA511	--	GGGCAACATAGTGAAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	--	AGCTGGATTATAACTCCCTCTTCTTTCTCTGGGGGGCCGTGGGGGCCGTGGGGCGGAGAGGTGCCGTT GGCCCCCCGTTGCTTTCTGCTTTCTCTGGGGAAGGATGCGCCACGCTGGGGAGAACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGGATGCGGGGGAGATGTGG GCGCGCGCGCCCGGGGCGCGGGCCACCGGGCCATCTTCTCCTCCCA
ESTD-BCR	--	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GACCAAAGAGGTCAGCTTCTGTTGTCCCGGGAAAGGGGCAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGCCCATCTGCCACA
ESTD-BRCA1a	--	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAAGATCGTACTGGTGTAGCAGTATTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	ACTAAATGTAAGAAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTCGTGTTTTAGCAAAGCGTCCAGAAAGGGAGGAG CTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	ACACAGGTGCTGGCCACTGGGGCTGGGGGATCCTCCTCCCCTAATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	--	CCCAGTCAGTTTGGGGGACCAGCAGCCATGCCACTGCACTCGAGCCTCTGGTGAGCCTTCAACCATGCATTCCATCTAA GCTCTGCAAAT

ESTD-C7	...	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	...	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATAATGAGGAGAGACATCACCTGGAATGTTAG GCAGTTGCCTAACTGGGGGGATGGACAGACAATGGCCACACCCATAGGGCGGATACAAAGAC AGGCAAGGAAGGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	...	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACATACACAGAGGACCCCTACCAGGACCAGAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	...	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGCTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTGCACAGACCCGCAGCCCTCAGGAG
ESTD-CB25	...	GTTTTCTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAAACAGGCATGGAGAATCCACGGGCGGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACACTGTCTGTTCTGTCAACAGAGTCTTACCGGTCCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	...	TTTTCTGTTCCCTGAAGATTGAGCTCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAT TGTGTGTTGGGCCTGGTTGCATTTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCCTCTTCTCTCCACCCAATGCTGCT TTCTCCGTGTTCATCCTGATGGAAGTCCTCAAACACCATTTCCATACC
ESTD-COL2A1c	...	AGAATGTATATAGTCCTCAAACTGCCATCTCCATTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTTCCTGTCACTTTCAGGGTGTTCAAGGTGGAAAGGT GAACAGGGTCCCGTCGGTCCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	...	TGAGAGAACACCTAGTCCTCCATCCTCTCTCTCAAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACACTGGACTCTTTCTTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAATGGCAAAGATATACAATACAATTTTATTTGACCAAACACTATCATCATGGAACAGC ATT
ESTD-CPT2	...	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAGATTAACTTCGTGGGCAGCAGATGAAAAAGTCACCACCATCCTCCTCATCATGAAAAC TGGGAGGCCGGGCCACATAGTCCGTGTAATCCCAGCATTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT

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ESTD-CTLA-4	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCCAC TCTCCTGTTTTTCTTCTCTCTGTCTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	CAGGGCCAGCGTGGTGGTCGAGCTGGTCACCATCCCGGCAGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATCATTGAAGCTGCTCTCAGGGGTTCCCCTTGGCCTGAGCCGAGGCCGAGAGCATACTCGG
ESTD-D11S1873	AAAAAAACATTTTAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCAATTACTTGCCAATTCATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD-D17S33	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTCGCACACATCCCAGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCTCTCTGGGGCGGGTG GGGTTGTGTGGCTATGTGGTCTTGTGTGTGAGACGGGGGCTTTGGTTGTTCAGTTGCCACTATTGCGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTGATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCA GGAGGCGGAGCTTGCAGTGAGTCCGAGATCGCCACTGCACTCACACCACTGCGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD-D3S11	AACTGATTAGAACCTGAAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAATCCAATAAAGTACACTGTAATAAAGAATTAACAGAATATCATTGT TTATTCAAAACTATTTATCCACTTATTTTATTGGTAAGCCATATCAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	AGGTTCCACATTATTGCTGATGTTGCTGACTGTTCCAGGAGGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTCAAAAACTCTCTACAGCCGTTGTTGTTATTAATTCAAGGTTGA ACATAAAGTA
ESTD-D3S2	GATCATGTGGCCCAAGTGGCGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACACGCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGGATGG CAGGTATGAAATATAATAAATCGTCCTTTATTGGAAGGATGCCGGTATGT
ESTD-D4S338	TTTTTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCTATATGGCAGGTATATGAAATGTATTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-D4S95	CTTTCATGCACGATAGGCCTTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTTCTTTTCTTTCTTAGAGTCTACCGG

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ESTD-D7S399	TGAATCTTAATTGCTATCTCTACAAAATGTATAAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTCACAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAAACATTTC
ESTD-DM	GTGGGGACACCGAGGGCTCCAGCCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGGAGTGGGGAGGGAGGACA GAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGGCCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGCGAAGAGAACAGAGT
ESTD-DRD1	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	TCTGCCTTTGGTCCAGGAGGCTGCCCGGGAGCCCAGGAGCTGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCCGGTACAGCCCCATCCCACCCGCACCACCGACTCTCCCCGACCCG TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAAGACCATGCCCAATG
ESTD-DRD3	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGCATAGTAGGCATGTGGGCGGGCCTGGCTGG CACCTGTGTGGGAGTTCTCTGCCCCACAGGTAGTTCAGGTGGCCACTCCAGCTGGCTCAGAGATGCCATA GCCCAGAGGGAGGTGCGTGATCGCCAAGGGGCTTCCTGTGGAGGA
ESTD-ERBB2	TCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATCGCTCCGCTCCCGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGTGGGGTCAGTGCGGGGCCCGGTCAGACCCCACCGCGGGGCTGGGAGGACTTCACCC CGCCCTCACCTCGTTTCCTCGCAGCAGTCTCCGCACGTGTACT
ESTD-ETS2	ACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAAGAGGCACCAGGAAGCACGTCCTGGCGCCTGGCA GTCCGTGGGACGGGGATGGTTCTCGGCGTGTTTGAGATTCTCAAAGGAGCGAGCCATGTCGTGGACACACAC AGACTATTTTAGATTTTCTTTTGCCTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAGAGG GTAGGAGGGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	GATAAGTACACTGAGGCGCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGCCCTCCAAGCCCGTAGGGGAACTGGGGGGATCTAGGGGTGAGGAATGGCCC AGCCCAGTCCCGGCCCGGTGCCTGGGTCCCAACAGAGGAGGGCCGTGGGAGGAGGACAGGAGGATGGGGC TGGGATGAG
ESTD-F9	AGATCCTGATGATTTTTTTCCTATTTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTCCATA GGTATGTGTCCAATTTATCCAGCACAATTTGTTAAAAACAAAAAC

ESTD-GCDH	⋮	CGCAGACCGGTCAGTGTGGGGTCGGGGAGTGTGGAGGAGGAGGAAGGAGGAGGAGGAACTGGGGGTTTAGGGGACT TTCCGGGGGTGACTTTCCCGGTTCTGGTGTTCTGGTGCACCGTGTGTTCTGCTGCCCCTGTTCAGCTGTCTGCGCAGTCGA GTGTAAGGGGACCCTCTGGTCGCCACCGTGTGTTCTGTGCTGCTGTGTTCGGGGAAATTCCGAGAGCT CTCTGTCCCGGAAATTCCGAGAGCT
		GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCACCCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCGCCTGAGCCCCAGGACAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD-GCK	⋮	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-GNAT2	⋮	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD-GPPK2L	⋮	CTGGGCTCGCCCCGCAGCAGCTGCTGGCCACCTGGACGCGGCGGGCCCAGGCTCACCTCTATAGTGGGGGTCG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-HRAS	⋮	TTGGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCCTGGGCGCCCACATTCTGGCCTTG AGGGCCCTGCGAGGACCCCAAGAGAGGCCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCCAAAGCTATGATAAACCTTAATTACACCCTGAGCAAAGAGTTCGGGCCTCCGGGCTTGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATTGGGATTGGCTTCCTGCTG
ESTD-HSD3B1	⋮	GGGCTAAAATTTCCGAGCAACTTGCATAGACTGTTTATTTGACTTGACACAGGATTGCTAGAGATAGG CAGGGAGGAGGAAGAGATGTGTTACAGTTTGTCAGAGAGAATAAAAGGATAAACCTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAAACGGTATACAGGGACACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT2	⋮	ACCAACGAGCGCGCGATACAGACACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCCTTCTATCGGCAAGAATGCGTACTTATTTGAAATAGTAGAGGTAA ACCACACGCCCCAAGAGTCACTGGACTGGCAGCTTCTGCAGCAGGCGGTGAACCCCCGTAGCCTAAA TGACAGCCGAAGAGGGCGCCGAAGACATGCAGATGTGC
ESTD-HT4	⋮	AACACACAAGCCCCAGCCAGGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCGTGTGGTTTTCTTCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTGAAAAGGTTCT
ESTD-HT5	⋮	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAAGATGTTC CAGGGCCACACATAGCTTAGTGGAGACTC
ESTD-IGFBP1	⋮	

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ESTD-IGHV4-6	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATTCATTATTATTATTATTTTTG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCCTCACTGCAAGCTCTG CCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTCCCTGTGTATTGAGGGGTGT GGGTCTCTACCTTGGGTGCGTGTTCTCTGCCTCAGGAGCTCTGTCTGTCAATTGCAGG
ESTD-KRT10	CCAAAGTTAAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTGCAGTGTTACCTTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTTTAAATAGTCTC TGCCCAGATACATCTCCCCTATATAGTTATTAACCAGTATTGATA
ESTD-KRT8	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGACATGAGAAGACCTCAGAGACGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD-LF79	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAATTTCCAATATGTAGTGCTGTTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAGGAGGGCTTCCCTTACCACCCAGA
ESTD-LMP2	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	TGTCAGTGTCCCCTAGGGGCACCTCACCACTCCCAGCTTCTTCAGCTTCTCATCTTTAGCACTGCTGCCTGCA AGGGTTTTGCTTAATTCTCAATTCAATGTCTCTTCATCTTTAATTATAAAAGAGATGTATCTAAACAAATAGAG TTCTGTTTTTGCTTAGTATCTGACTACTTTTATTATAAAAATTTTTCACCTG ATTGTTATCAGAAGTTCACACAATTATTAAAAATTTTTCACCTG
ESTD-MCC	TTGTCAGGAGTGTGCTGATGTGCTGCCTCCCCAGCTCTGTCCCTAGCCGAACTTCAGGACAACGTGCAG
ESTD-METH	CATCCCATGTAGGAGGAGGAGCCTTAGTCAAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTTCCCAAGGGGTTTGGTCTAAGTTGCTAAGTTGCTGATTACCCGGAATTTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTTAGCATGG
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Label	Sequence
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ESTD-OTC	GTGACCTTCTCACTTTAAAAAACTTTACCGGAGAAGAAATTAAAATATATGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGGAGAGGTATGTAACA
ESTD-PAI1	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGCAACAGGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGGAGTCAGCACCGTGTATCATCGGCGAGGCGGCCGCGGCAC ATGGCAGGGGATGAGGGAAAGACCAAGAGTCCCTCTGTTGGGCCCAAGTCCTAGACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAATTTAGTTAGAAGGAATCGAAACTGCTGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTTCTCACTTTCTGTGTTCTAGAAACGTTTTCTAG GACTGGCAGTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCC
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ESTD-RDS

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ESTD-RYR1

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ESTD-SSA1

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ESTD-THRB

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ESTD-TNFA

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ESTD-TYR

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ESTD-VB12	--	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCAAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTCTTTACTCTCTGCCTGCAGGATGTG CGACGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCCAGTGAGAAACGCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	--	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST717770 6	--	AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAGCTGTGTGGTGGAAGG AGTGCCCAGTCCAGTCCAGGGTGACACTGGACAAGAAAGAGGGCCATCCAAGG
EST52418 6	--	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGAGATGTCG GGGAGTGGCGCGGGAGTTGGGCGGAGTACGGGCCTGCAGGCCATACACTAAAGTGAAAACTGTGAGTGTGG
EST13586 3	--	CCCACTCTATTTGCCCAGCCCCAGGGACACAGAGCTGATCCTTGAACTCTTAAGTTCCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTTATCAGCCTCCCAGCCCCAGACCCTGGCTGCAGACAT AAATAGGCCCCTGCCAAGAGCTGCCTGCTTAGAGACTGCGGAGAAGGAGAGGAGGCCTCTGCCTGCCCCG GTCACTC
EST51976 7	--	AGGCAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCCACTTGAGCTTCCTGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGGACAAGAGACTCTCTCCCT CCCTGAGCTGCTGAGCAACAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGTGCAGAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCCTGGTGC

EST114586	--	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCAGTGTTGCTATTGCAGGACGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCCATTAAAAACATTCTATGAGCCAGGAGAAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST398528	--	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST624480	--	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCGTCTTGGCATTGCCGGCCCTCCTGGGCCCCGTGG TCCTCTGGTGCTGTGGGGTAGTCCTGGAGTCAAGCGGTGCTCCTAGTGAAGCTGGTCGTGATGGCAACC CTGGGAACGATGGTCCCCCAGGTCGCGATGGTCAACCCGGACCAGTTGCTCAACCCGGACAAGGGAGAGCGCGGGTTACCCTGG CAATAT
EST360272	--	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACACAGCATTGCATACATGGATGAAGCTGGAAACCTGAAAAAGG CTGTCATTCTTACAGGGCTCTAAATGATGTTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGCTGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAA
EST122740	--	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST768078	--	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCACTCAATGGGCCCAGTCAGGCCCGGCTCCGGAGGACTCACCACTGCCCCCCT GCTGCCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST444387	--	GCAGCCAGGAGCCGCTGCACCATGCCCCCGCATAGATGCGGACTTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG
EST128393	--	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTACTATGAATATTATGATACTTAGCTTAG
EST544198	--	CTTCTGCCTAATTTGAATGATGTATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTATTTGGGTTTAGCGTGGTCGTATGTGTCTACTA TAGTCCAAGTGAA

EST10398 2	--	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCACCAATAGTGTCTATTAGGCATTTG
EST36751 7	--	CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACTTAGTTTTCTGATCTATGGTTCAAGTTAAACAG
		CACGTGGAAAGGAGCTATTTTTGGAGGCTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGAGTTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAAATAAATG AAGGATTTGACCTGCTCTGCGCTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCTA
EST40562 3	--	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTCATGCAGCGTGTGACAGGATGGAAGACTGGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGGCTCTGGC CCTAGGACTTAGTATCC
EST18288 3	--	TTCCCGCCCAGCCCCCATCCTTGGCCACCCTGGTCCCCCTCAGGGGCCCACCCCGCGGGGCACTCACCGCTCT CGCTCTCGGTAACATCCGGCGGGGCGTCCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCCCTTCCTGTCCCGGGCCCTTGCCAGGGGCCCAGGCCCCAGGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGGAGTGTGTCTCCCACGTG
EST70523 3	--	CAGTGTATCTGGAAAGCCTACAGGACACCAAATAAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCCGAGAAGATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAAACCTT
EST58707 7	--	AGACCATGAAGAGGAGTTGAAAGGCCTACAAATCGGAAACTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCGTGTCCAAGGAGCTGCAGGGGCGGCGCGGGACATGGAGGA CGTGCGCGGGCGGGCCTGGTGCAGTACCGGGGGCGAGGTCGCAGGCCCCGGCGCCGAGCACCGAGGAGC TGCGGGGTGCGGGCTCGCGCTCCCACTGCGCAAGCTGCGGTAAGCGGGCTCCTC
EST74167 6	--	CGCCTGGGTGCAGTACCGCGGGGGCAGGGTGCCAGGGTGACGGGAGGCAGCACCGAGGAGAGCTGCGGGGTGCG CCTGGCCTCCCACCTGCGGCGAAGCTGCGGTAAGCGGCTCCTCCCGGGAGCTGCGGGATGCCGGGCTGCAGAAGCGGCC TGGCAGTGTACCAGGCGGGGGGCGGGGGGCGGCGGCGGCCCTCAGCGGCCATCGGGCGGGCGGCCATCCGGCGAGCCCCTG GGGCGCCGGGTGGAACAGGGCGGCGGGCGGCGGCGGGCGCCCACTGTGGCTC
EST43211 8	--	TGTAGCCAAAGTCACCTGCATCATCATTGGCTGGCAGGCTTGGCCAGTTTGTGCTGGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCCTCCCGATAGGGCTGGGCCTGACCAAAAATATACTGGGTTTCCTTTTCTGTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCCTAAAGAGAGGCTTATG
EST36770 4	--	

EST ID	Sequence
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EST201182	GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGGCTGTGTGGTCCAGCT GAGGTGAGGGGCCTTGAAGCTGGGAGTGGGGTTTAGGGACGACGCGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGACGCGGGTCTCTGCGTCCTAAGCT CTGAGA
EST530186	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAGGAGGCCACGAGGGATCGAAGTTAGTGAAGTC
EST687875	CTTCCTATGGGATTTGACTTTATTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACACTTTCGAAACATTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
EST340882	GTGGGGGCAACAGTGGGAGAGAAGAGGGCCCAGGGTATAAAAGGGGCCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCGAACCACTCAGGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
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EST453110	GCCCTCCTCTTCCAATTCTGTCCTATAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACACAAACACACAGCATTGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAATCACCTCTTTCATTTAACAGCCCTTATTCAAACAGCCCTTATTCAAACTGTGTCATTTGTTGAAT

EST	Sequence
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EST68308 5	GGAAAGAGATTAAGAAGCTTGATTTGGACAATTCTGGTTCTTGAGTGTGGAAGAGTTCATGTCTCT GCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	GGAATATTAAAAATATTTTAAAATACCTCCATTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGTCAATTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTTGCCTTGAATTGGATTTTTAATGTTGACTTTATCAT
EST52908 0	ATCACAGGTCTCTGGTCTCTGGCCATCATTCCTGGGAGAGATGGATGGGTCTGCCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590	AGGAGAAGCTGAGGAGGGGAAGAGAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAAATGAC
EST76136	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	CTCTGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGACAACAAGGACAGCCACATGGCGGGCGATGGCGCCCGGGAGTTCTGGT TGCGGCCACGCGTGTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGGATGCGTAAACCTTTGTTTCT TGGCCCAAGGAGGGGCGCGGGGTGCCATGCCTGAGATGTAGATGCGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5   various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table, or a portion thereof which includes a polymorphic site, or the complement of the segment or portion thereof.

2. The nucleic acid segment of claim 1 that is DNA.

3. The nucleic acid segment of claim 1 that is RNA.

4. The segment of claim 1 that is less than 100 bases.

5. The segment of claim 1 that is less than 50 bases.

6. The segment of claim 1 that is less than 20 bases.

7. The segment of claim 1, wherein the polymorphic site is biallelic.

8. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is the reference base for the fragment listed in the Table, column 3.

9. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is an alternative form for the fragment listed in the Table, column 4.

10. An allele-specific oligonucleotide that hybridizes to a segment of a fragment shown in the Table, column 7 or its complement.

11. The allele-specific oligonucleotide of claim 10 that is a probe.

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12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.

13. The allele-specific oligonucleotide of claim 10 that is a primer.

14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.

16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.

17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.

18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.

19. The method of claim 18, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6   C12Q1/68   C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6   C12Q   C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document ---	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract --- -/--	1-20

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
17 June 1998	2 3. 09. 1998

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Knehr, M

International Application No

PCT/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMEST10 embl Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence * ---	1-3,10, 11
X	SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS,USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1 ---	1-3, 7-10,13, 14,17-20
X	FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3 ---	1-3,7-9, 17-20
X	HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN RACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document ---	10-16, 18-20
X	GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document ---	18-20

-/--

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document -----	18-20

INTERNATIONAL SEARCH REPORT

Box I	**Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II	**Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

   ### 1-20 (partially)

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

1. Claims: 1-20 (partially)

> INVENTION 1: An isolated nucleic acid segment including a
> polymorphic site having the nucleotide sequence of SEQ ID
> NO:1149, or the complement of that segment or portions
> thereof, an allele-specific oligonucleotide probe or primer
> hybridizing to such a segment or its complement, and a
> method of analyzing such a nucleic acid by determining the
> bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

> INVENTION 2 to INVENTION 2669:
> -Idem as invention 1 but limited to the sequences having SEQ
> ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID
> NO:1150, invention 3 is limited to SEQ ID NO:1151, ...,
> invention 2269 is limited to SEQ ID NO:3817).
>
> For the sake of conciseness, the first group is explicitedly
> defined, the other groups are defined by analogy hereto.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98
FR 2722295 A	12-01-96	NONE	